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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## 5 (i) APPLICANT:

(A) NAME: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL  
RESEARCH ORGANISATION

(B) STREET: Limestone Avenue

(C) CITY: Campbell

10 (D) STATE: ACT

(E) COUNTRY: AUSTRALIA

(F) POSTAL CODE (ZIP): 2612

(A) NAME: THE AUSTRALIAN NATIONAL UNIVERSITY

15 (B) STREET: BRIAN LEWIS CRESCENT

(C) CITY: ACTON

(D) STATE: ACT

(E) COUNTRY: AUSTRALIA

(F) POSTAL CODE (ZIP): 2601

20 (A) NAME: GOODMAN FIELDER LIMITED

(B) STREET: LEVEL 42, GROSVENOR PLACE

(C) CITY: SYDNEY

(D) STATE: NSW

25 (E) COUNTRY: AUSTRALIA

(F) POSTAL CODE (ZIP): 2000

(A) NAME: GROUPE LIMAGRAIN PACIFIC PTY LIMITED

30 (B) STREET: LEVEL 31, 1 O'CONNELL STREET

(C) CITY: SYDNEY

(D) STATE: NSW

(E) COUNTRY: AUSTRALIA

(F) POSTAL CODE (ZIP): 2000

35 (ii) TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS

(iii) NUMBER OF SEQUENCES: 17

## 40 (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## 45 (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "pcr primer based on the N-terminal sequence of wSBE I 5' end at position 168 of SEQ ID NO:5"

55 (iii) HYPOTHETICAL: NO

per  
paper  
#10

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(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

- 5 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: triticum tauschii  
 (F) TISSUE TYPE: Endosperm

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 GGCACGCGAG AGACTGG 17

(2) INFORMATION FOR SEQ ID NO: 2:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "pcr primer in which 5 ' end is at position 1590 of SEQ ID NO:5"

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

- 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: triticum tauschii  
 (F) TISSUE TYPE: Endosperm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 35 TACATTTTCCT TGTCCATCA 19

(2) INFORMATION FOR SEQ ID NO: 3:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "pcr primer 5 ' end is at position 1 of SEQ ID NO:5"

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

- 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: triticum tauschii  
 (F) TISSUE TYPE: Endosperm

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ATCACGAGAG CTTGCTCA 18

5 (2) INFORMATION FOR SEQ ID NO: 4:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "pcr primer 5 ' end is at position 334 of SEQ ID NO:5"

15 (iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE:  
(v) FRAGMENT TYPE:  
20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: triticum tauschii  
(F) TISSUE TYPE: Endosperm

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
CGGTACACAG TTGCGTCATT TTC 23

(2) INFORMATION FOR SEQ ID NO: 5:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2687 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
30 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
40 (iv) ANTI-SENSE:  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: triticum tauschii  
(F) TISSUE TYPE: Endosperm  
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
ATCGACGAAG ATGCTCTGCC TCACCGCCCC CTCCTGCTCG CCATCTCTCC CGCCGCGCCC 60  
50 CTCCCGTCCC GCTGCTGACC GGCCCGGACC GGGGATTTTCG GCCAAGAGCA AGTTCTCTGT 120  
TCCCGTGTCT GCGCCAAGAG ACTACACCAT GGCAACAGCT GAAGATGGTG TTGGCGACCT 180  
TCCGATATAC GATCTGGATC CGAAGTTTGC CGGCTTCAAG GAACACTTCA GTTATAGGAT 240  
55 GAAAAAGTAC CTTGACCAGA AACATTTCGAT TGAGAAGCAC GAGGGAGGCC TTGAAGAGTT 300  
CTCTAAAGGC TATTTGAAGT TTGGGATCAA CACAGAAAAT GACGCAACTG TGTACCGGGA 360

ATGGGCCCCCT GCAGCAATGG ATGCACAACCT TATTGGTGAC TTCAACAACCT GGAATGGCTC 420  
 5 TGGGCACAGG ATGACAAAGG ATAATTATGG TGTTTGGTCA ATCAGGATTT CCCATGTCAA 480  
 TGGGAAACCT GCCATCCCCC ATAATTCCAA GGTAAATTT CGATTTCCACC GTGGAGATGG 540  
 ACTATGGGTC GATCGGGTTC CTGCATGGAT TCGTTATGCA ACTTTTGACG CCTCTAAATT 600  
 10 TGGAGCTCCA TATGACGGTG TTTACTGGGA TCCACCTTCT GGTGAAAGGT ATGTGTTTAA 660  
 GCATCCTCGG CCTCGAAAGC CTGACGCTCC ACGTATTTAC GAGGCTCATG TGGGGATGAG 720  
 TGGTGAGAGG CCTGAAGTAA GCACATACAG AGAATTTGCA GACAATGTGT TACCGCGCAT 780  
 15 AAAGGCAAAC AACTACAACA CAGTTCAGCT GATGGCAATC ATGGAACATT CCATATTATG 840  
 CTTCTTTTGG TACCATGTGA CGAATTTCTT CGCAGTTAGC AGCAGATCAG GAACACCAGA 900  
 20 GGACCTCAAA TATCTTGTTG ACAAGGCACA TAGCTTAGGG TTGCGTGTTT TGATGGATGT 960  
 TGTCCATAGC CATGCGAGCA GTAATATGAC AGATGGTCTA AATGGCTATG ATGTTGGACA 1020  
 AAACACACAG GAGTCCTATT TCCATACAGG AGAAAGGGGT TATCATAAAC TGTGGGATAG 1080  
 25 TCGCCTGTTC AACTATGCCA ATTGGGAGGT CTTACGGTAT CTTCTTTCTA ATCTGAGATA 1140  
 TTGGATGGAC GAATTCATGT TTGACGGCTT CCGATTTGAT GGAGTAACAT CCATGCTATA 1200  
 30 TAATCACCAT GGTATCAATA TGTCATTCGC TGGAAATTAC AAGGAATATT TTGTTTGGGA 1260  
 TACCGATGTA GATGCAGTTG TTTACATGAT GCTTGCGAAC CATTTAATGC ACAAATCTT 1320  
 35 GCCAGAAGCA ACTGTTGTTG CAGAAGATGT TTCAGGCATG CCAGTGCTTT GTCGGTCAGT 1380  
 TGATGAAGGT GGAGTAGGGT TTGACTATCG CTTTGCTATG GCTATTCCTG ATAGATGGAT 1440  
 TGACTACTTG AAGAACAAAG ATGACCTTGA ATGGTCAATG AGTGCAATAG CACATACTCT 1500  
 40 GACCAACAGG AGATATACGG AAAAGTGCAT TGCATATGCT GAGAGCCACG ATCAGTCTAT 1560  
 TGTTGGCGAC AAGACTATGG CATTTCTCTT GATGGACAAG GAAATGTATA CTGGCATGTC 1620  
 45 AGACTTGCAG CCTGCTTCAC CTACAATTGA TCGTGGAATT GCACTTCAAA AGATGATTCA 1680  
 CTTCATCACC ATGGCCCTTG GAGGTGATGG CTACTTGAAT TTTATGGGTA ATGAGTTTGG 1740  
 CCACCCAGAA TGGATTGACT TTCCAAGAGA AGGCAACAAC TGGAGTTATG ATAAATGCAG 1800  
 50 ACGCCAGTGG AGCCTCTCAG ACATTGATCA CCTACGATAC AAGTACATGA ACGCATTTGA 1860  
 TCAAGCAATG AATGCGCTCG ACGACAAGTT TTCCTTCCTA TCGTCATCAA AGCAGATTGT 1920  
 55 CAGCGACATG AATGAGGAAA AGAAGATTAT TGTATTTGAA CGTGGAGATC TGGTCTTCGT 1980  
 CTTCAATTTT CATCCCAGTA AAACCTTATGA TGGTTACAAA GTCGGATGTG ATTTGCCTGG 2040  
 GAAGTACAAG GTAGCTCTGG ACTCCGATGC TCTGATGTTT GGTGGACATG GAAGAGTGGC 2100  
 60 CCAGTACAAC GATCACTTCA CGTCACCTGA AGGAGTACCA GGAGTACCTG AAACAACTT 2160  
 CAACAACCGC CCTAATTCAT TCAAAGTCCT GTCTCCACCC CGCACTTGTC TGGCTTACTA 2220  
 65 TCGCGTCGAG GAAAAAGCGG AAAAGCCTAA GGATGAAGGA GCTGCTTCTT GGGGCAAAGC 2280  
 TGCTCCTGGG TACATCGATG TTGAAGCCAC TCGTGTCAAA GACGCAGCAG ATGGTGAGGC 2340

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GACTTCTGGT TCCAAAAAGG CGTCTACAGG AGGTGACTCC AGCAAGAAGG GAATTAAGTT 2400  
 TGTCTTCGGG TCACCTGACA AAGATAACAA ATAAGCACCA TATCAACGCT TGATCAGAAC 2460  
 5 CGTGTAACGA CGTCCTTGTA ATATTCCTGC TATTGCTAGT AGTAGCAATA CTGTCAAAC 2520  
 GTGCAGACTT GAGATTCTGG CTTGGACTTT GCTGAGGTTA CCTACTATAT AGAAAGATAA 2580  
 10 ATAAGAGGTG ATGGTGCGGG TCGAGTCCGG CTATATGTGC CAAATATGCG CCATCCCGAG 2640  
 TCCTCTGTCA TAAAGGAAGT TTCGGGCTTT CAGCCCAGAA TAAAAA 2687

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 807 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE:

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: triticum tauschii  
 (F) TISSUE TYPE: Endosperm

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(ix) FEATURE:

- (A) NAME/KEY: Protein  
 (B) LOCATION: 1..807  
 (D) OTHER INFORMATION: /label= sbel  
 /note= "deduced amino acid sequence from SEQ ID NO:5"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Cys Leu Thr Ala Pro Ser Cys Ser Pro Ser Leu Pro Pro Arg  
 1 5 10 15  
 40 Pro Ser Arg Pro Ala Ala Asp Arg Pro Gly Pro Gly Ile Ser Ala Lys  
 20 25 30  
 45 Ser Lys Phe Ser Val Pro Val Ser Ala Pro Arg Asp Tyr Thr Met Ala  
 35 40 45  
 Thr Ala Glu Asp Gly Val Gly Asp Leu Pro Ile Tyr Asp Leu Asp Pro  
 50 55 60  
 50 Lys Phe Ala Gly Phe Lys Glu His Phe Ser Tyr Arg Met Lys Lys Tyr  
 65 70 75 80  
 Leu Asp Gln Lys His Ser Ile Glu Lys His Glu Gly Gly Leu Glu Glu  
 85 90 95  
 55 Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr Glu Asn Asp Ala  
 100 105 110  
 60 Thr Val Tyr Arg Glu Trp Ala Pro Ala Ala Met Asp Ala Gln Leu Ile  
 115 120 125

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	Asp	Tyr	Arg	Leu	Ala	Met	Ala	Ile	Pro	Asp	Arg	Trp	Ile	Asp	Tyr	Leu
	465					470					475					480
5	Lys	Asn	Lys	Asp	Asp	Leu	Glu	Trp	Ser	Met	Ser	Ala	Ile	Ala	His	Thr
				485						490					495	
	Leu	Thr	Asn	Arg	Arg	Tyr	Thr	Glu	Lys	Cys	Ile	Ala	Tyr	Ala	Glu	Ser
			500						505					510		
10	His	Asp	Gln	Ser	Ile	Val	Gly	Asp	Lys	Thr	Met	Ala	Phe	Leu	Leu	Met
			515					520					525			
	Asp	Lys	Glu	Met	Tyr	Thr	Gly	Met	Ser	Asp	Leu	Gln	Pro	Ala	Ser	Pro
15		530					535					540				
	Thr	Ile	Asp	Arg	Gly	Ile	Ala	Leu	Gln	Lys	Met	Ile	His	Phe	Ile	Thr
	545					550					555					560
20	Met	Ala	Leu	Gly	Gly	Asp	Gly	Tyr	Leu	Asn	Phe	Met	Gly	Asn	Glu	Phe
				565						570					575	
	Gly	His	Pro	Glu	Trp	Ile	Asp	Phe	Pro	Arg	Glu	Gly	Asn	Asn	Trp	Ser
			580						585					590		
25	Tyr	Asp	Lys	Cys	Arg	Arg	Gln	Trp	Ser	Leu	Ser	Asp	Ile	Asp	His	Leu
			595					600					605			
	Arg	Tyr	Lys	Tyr	Met	Asn	Ala	Phe	Asp	Gln	Ala	Met	Asn	Ala	Leu	Asp
30		610					615					620				
	Asp	Lys	Phe	Ser	Phe	Leu	Ser	Ser	Ser	Lys	Gln	Ile	Val	Ser	Asp	Met
	625					630					635					640
35	Asn	Glu	Glu	Lys	Lys	Ile	Ile	Val	Phe	Glu	Arg	Gly	Asp	Leu	Val	Phe
				645						650					655	
	Val	Phe	Asn	Phe	His	Pro	Ser	Lys	Thr	Tyr	Asp	Gly	Tyr	Lys	Val	Gly
			660						665					670		
40	Cys	Asp	Leu	Pro	Gly	Lys	Tyr	Lys	Val	Ala	Leu	Asp	Ser	Asp	Ala	Leu
		675						680					685			
	Met	Phe	Gly	Gly	His	Gly	Arg	Val	Ala	Gln	Tyr	Asn	Asp	His	Phe	Thr
45		690					695					700				
	Ser	Pro	Glu	Gly	Val	Pro	Gly	Val	Pro	Glu	Thr	Asn	Phe	Asn	Asn	Arg
	705				710						715					720
50	Pro	Asn	Ser	Phe	Lys	Val	Leu	Ser	Pro	Pro	Arg	Thr	Cys	Val	Ala	Tyr
				725						730					735	
	Tyr	Arg	Val	Glu	Glu	Lys	Ala	Glu	Lys	Pro	Lys	Asp	Glu	Gly	Ala	Ala
			740						745					750		
55	Ser	Trp	Gly	Lys	Ala	Ala	Pro	Gly	Tyr	Ile	Asp	Val	Glu	Ala	Thr	Arg
			755					760					765			
	Val	Lys	Asp	Ala	Ala	Asp	Gly	Glu	Ala	Thr	Ser	Gly	Ser	Lys	Lys	Ala
		770					775					780				
60	Ser	Thr	Gly	Gly	Asp	Ser	Ser	Lys	Lys	Gly	Ile	Asn	Phe	Val	Phe	Gly
						790					795					800

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Ser Pro Asp Lys Asp Asn Lys  
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- (2) INFORMATION FOR SEQ ID NO: 7:
- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE:
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: triticum tauschii  
 (F) TISSUE TYPE: Endosperm
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_signal  
 (B) LOCATION: 1..319  
 (D) OTHER INFORMATION: /function= "3' untranslated region  
 of wSBE I-D4 cDNA"
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
- |    |  |     |
|----|--|-----|
| 30 | GCGACTTCTG GTTCCAAAAA GGCGTCTACA GGAGGTGACT CCAGCAAGAA GGGAATTAAC  | 60  |
|    | TTTGTCTTCG GGTCACCTGA CAAAGATAAC AAATAAGCAC CATATCAACG CTTGATCAGA  | 120 |
|    | ACCGTGTACC GACGTCCTTG TAATATTCCT GCTATTGCTA GTAGTAGCAA TACTGTCAA   | 180 |
| 35 | CTGTGCAGAC TTGAGATTCT GGCTTGGACT TTGCTGAGGT TACCTACTAT ATAGAAAGAT  | 240 |
|    | AAATAAGAGG TGATGGTGCG GGTCGAGTCC GGCTATATGT GCCAAATATG CGCCATCCCCG | 300 |
| 40 | AGTCCTCTGT CATAAAGGA   | 319 |
- (2) INFORMATION FOR SEQ ID NO: 8:
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4890 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- 50 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE:
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: triticum tauschii  
 (F) TISSUE TYPE: Endosperm
- 55 (ix) FEATURE:

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**POLICE**

	TAGAGTAGGG	AGGAGAGGCT	GGTGCATGAT	ACATGGTGGA	CTAGCCCATA	TATTTACCCC	1800
	TCCCCACCC	ACTAACAAGT	TTTTTTTATT	AGGTCTTCAT	CCTCTGATTT	GTTTTTCTGT	1860
5	TAGCCCATTC	TTCATCATGG	ACTTATTAAT	CATGATTAGT	TTCTTGGATT	TTTGTTTACT	1920
	TGACTTGAAT	TTGACAATGT	GCCTCATATA	TGGCATGTGG	GA CTGATAGG	AAGATATATT	1980
10	CTCACAACAT	TAACTTAAAA	AGGATTATTT	TTTGGTGCA	GTCGTAAAGA	AAACTACTTT	2040
	CTTTTATGCT	AAAAGTTATT	CAAACATAGA	TTTATAACA	AAGGATATCA	CCATGCATGA	2100
	CCATGCGCTC	TCTCATGTTT	ACTCTAGAAA	CCATATATCT	CTTTGTTGCA	AAATATTTAA	2160
15	TCTATCCTCC	TTGTTTCTGG	GAATGAGTCG	GGGAAGGTAA	TCTTAGGGAA	GGTTAAAGTG	2220
	AGGCAAGTAA	GAGCAACTCT	AGCAGAGTCG	CGATATGCCC	AATCGCCATA	ATGCCAATAT	2280
20	GGCATTTTTG	GCCCCAAATG	GCACTTCAGA	AGAGTCACCA	TATCCCTTCG	GATAGCCATA	2340
	ATTTAGGGAG	CTCGCTCCAC	AAACAAGCTT	CGAGCCTCCA	AATATGGAGG	CCATGGATTTC	2400
	GTTGTTTGCG	ACTCACTCCA	TATCCAACCG	CAAGCGCATG	CATGAGGGAA	GTTTTAGCTT	2460
25	CTTCCTCCTT	GCGCCAACGC	CGGGATTTTA	CACAGCGCAT	TACAGGTACA	TGAACCAGCA	2520
	TGCACAGATA	ATCACCGACG	AGTGGGGTGA	CAAGAAGGAT	AAGCACCCCTC	CCATTAGTGG	2580
30	TGCGCCCACT	CCCCTCAAAT	TCATGAGGCA	GCCATTTGGA	TGGTCATCGC	GTGGCATAAG	2640
	CTCCGACTAT	AAAATCTCAA	CGGCATCACC	AAAACCATAG	CTGCCGCCTC	CCCCTTCCTC	2700
	GGCATCACCT	CCCCAAGACA	TCTCCTCCCC	TCTATGCCAC	AATGTCATCA	TTATGGAGAG	2760
35	ACACAAC TAC	TGGTAAACCG	CATACCCAAT	CATGGTTTAC	CGGCAGTGCG	AACCCACCT	2820
	TCCTCCCACG	ATGGTAGGAT	ATTCTCCTCC	TAGAATGGCG	CGTGTGGCGC	TTCCTCCTCC	2880
40	CGAGGCTGAT	ATGTCGGCTC	CCATGATGGC	GTGCATCATT	GATTTGGCGC	TTCGGGTCCA	2940
	TCATACATGT	TAACGAGGTC	ATCCCCATTG	ATGTCGTTGG	TCCCCTTGCC	CCCCAGTCGG	3000
	ATCCTGAGGA	CCCGTTGAT	GTCGCAATGC	GACTCTCCAA	ACTCAAAGCT	CACAATGAGG	3060
45	AGTACGTCCT	CTAGGAGTTC	CGCCCCGCAA	CCATCTATAA	GGAGGAGCAA	CGATAGCTCT	3120
	CCCCTACGCC	TTCCTCGACG	ATCTCTCTTA	GGAGGACAAC	GGCTAGACGA	CGGCGGCGGC	3180
50	GGCGAAGGTA	CTGCAGGTAG	TAGAACATAG	CAATGTGCAA	TGGCGACATT	GCATATTTTG	3240
	AAAATGTGCG	TCAACGACTT	TTGAAGTCGC	AAATAAAATG	TAGTGTGACT	ACTTTTGGCC	3300
	AGCAATATAA	GTTTATCACA	TTTGATAATG	ATTTGAACCG	GTGTGGTTCA	ACTAAATGTA	3360
55	CCATAAATTG	AACATACAAA	TTTTTAGCAA	ATGAAAAAAG	AAACAAGTAA	GACCACAAAT	3420
	ATGAAAGCCG	CATATCGCGA	CTATGTGTTT	GAGCCGCAGC	TGCCAAGTAC	ATATGAAGCG	3480
60	TACTCCATAT	GACATACGAC	AACCATACAT	ATGAAGACTC	TACTAGAGTT	CTCTAAGGCC	3540
	GCTTTTAGCG	CCTTTCGTGC	AGTGGTGCCC	ATAGGGAGTG	AGGGTAGTTG	GA CTGTTCGT	3600
	TTCCCTTTT	TTCATTTCTT	TGAAATCTAT	TTTATTTTTT	TTCTCTTTTG	TAGGTTTCCC	3660
65	AAATTTATAT	ACCATTTTTT	TGTTTCTCGC	TATTTTTTGT	TGTTATATTC	TAGTTTCATA	3720
	TTTTTCTATT	ATTAATTTGT	GTCTCTTATG	AGAAGTCCAG	ACTTGCATAT	GGAGGTGCAC	3780

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ACACAAACAT ATAAAGTATA AATACTAACT TGAGAAGTAT GTTTGCGTGG TCAAAAAAAC 3840  
 5 ATCATCAAAA CCTGCCAATA TGAGATATAG TTTTGAATAT ATCAATATGA GCAACGCAAC 3900  
 CATTTAAAT GTGAACAATT GTTTTTTTAG AAAAAATATA AGAAATAACT CCAACCCAGC 3960  
 CAAACCACAT GCTATACACT TGCTCCATAT GAAACCATGT TTGCTATTGG GCAGTTGCCT 4020  
 10 GAAACCGAAA GTAATGTTAG CCGTTTTTCT ATTCAAAGAA GAAGGAGAGT CGAGGTGACG 4080  
 CGATGCTTAG ACGTGAGATG GGGATGACCA CAACGTCCCT ACAGAGACCT CACCGGAGAT 4140  
 15 GGGGACATTG CAGTTGACAC GAGAGCGGTG AGGGGCTGCG ATGCGTGTGC GGCAACATGT 4200  
 GGCGAGGCGG ACGTCGGGCT GGCAGGTAGG GGGGAGGGGG AAGGACCGGG GGAGGAAGAA 4260  
 GAGGAGTAGC CTGCAAAACA TGGTACACCA GTTTTCTGCC CTACGAAAAC CTCATTTTCAT 4320  
 20 TCCCCACCC TGACAAGCAA CAACCAACCA TCGCAGTCCC ACATGTCCCT CTGGTCTTTG 4380  
 CAAAAAGTAA TTGTTCTTGC TGGACAGCGC AAAGAGTAA CTTTTGTTAG TTTTCATTTTC 4440  
 TAGAAAAAGC AATCCTTTTA TAGTCTTTT GTGAAAGTAA TGCTTTTATA GTGATTGGGA 4500  
 25 TGTTCTTTTA GAGCAAATAT CTTCTTTTTT TTTTAGGGAA AAGAGCAAAT ATCTTCCACT 4560  
 TTTACAAAA CTGACGAAGG CTGAAAGTGG CGAGACAGTG AGGGCCATA GCTTTCGTCC 4620  
 30 GGCCAGCGG CGCACGACCG TCCACGTGCA CCGGCGCCCT CCGGGCCCG CAGATCCGTT 4680  
 CTCCCTCGCC CCCGTTTCCC CCTCCCTCCC TCTCGTTGCT TCCACTCCAC TGTTCTCCTC 4740  
 35 TTCTGTCCA AAGCGGCCAC GGACCGGAAA AAAATCACGC CTTTCCGTTG GGTCTCCGGC 4800  
 GCCACACTCC TCCTCCGGCC GATATAAAGC GCGCGGGGCC ACGGGCCCGG CGCAAAATGG 4860  
 GATTCCCGTC CGCCGCCATG GAGGAAGATG 4890

- 40 (2) INFORMATION FOR SEQ ID NO: 9:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 45 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: cDNA  
  
 (iii) HYPOTHETICAL: NO  
 50 (iv) ANTI-SENSE:  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *triticum tauschii*  
 55 (F) TISSUE TYPE: Endosperm  
  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1  
 60 (D) OTHER INFORMATION: /product= "coding region of wSBE I-D4 gene"  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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	ACGGGCCCCG	CGCAAAATGG	GATTCCCCGTC	CGCCGCCATC	GACGAAGATG	CTCTGCCTCA	60
	CCGCCCCCTC	CTGCTCGCCA	TCTCTCCCGC	CGCGCCCCCTC	CCGTCCCGCT	GCTGACCGGC	120
5	CCGGACCGGG	GATCTCGGTG	AGTCAGTCGG	GATCTTCATT	TCTTTTCTTT	TCTTTCGTTT	180
	CCGGCTCCGT	TCTGCCGGGG	TTTCCCTGAT	GCGATGCCGC	GCGCGCGCAG	GGCGGCGGCA	240
10	ATGTGCGGCT	GAGCGCGGTG	CCCGCGCCCT	CTTCGCTCCG	CTGGTCGTGG	CCGCGGAAGG	300
	TGAGCCCTCT	CCCCTGTCTA	CCCAGATTTC	CGACCGTGAT	CCCCTGTTGT	CGCCGGGCAA	360
	ACGGAATCTG	ATCCACGGTG	GTTATTGGAA	ATAGTATATA	CTACTAATAA	ACTTGAGGCT	420
15	GGGATTTCGT	CACTGAGGAA	CAAGTGGATG	CGATTTTCGAT	TGGATTTCCT	TGCTTTATGC	480
	GATCCGTACG	CAGAATATCC	CTCCTGCAGT	GTCTCAACCG	TATTACTGGA	TGTACAACCC	540
20	AAATGTGTAT	AATCTGTGCT	GAATGTATCA	ACCAATAATT	GCTGCATTGT	GAAAACATAA	600
	TCCTGTGTTG	TGTCTCTACT	ACTTGTTTCAG	TCCTGATCTG	CCGCTTATCC	TAACCTTTGT	660
	TCATTTATGG	AAGGCCAAGA	GCAAGTTCTC	TGTTCCCGTG	TCTGCGCCAA	GAGACTACAC	720
25	CATGGCAACA	GCTGAAGATG	GTGTTGGCGA	CCTTCCGATA	TACGATCTGG	ATCCGAAGTT	780
	TGCCGGCTTC	AAGGAACACT	TCAGTTATAG	GATGAAAAAG	TACCTTGACC	AGAAACATTC	840
30	GATTGAGAAG	CACGAGGGAG	GCCTTGAAGA	GTCTCTCTAA	GGTTAGCTTT	TGTTTCATGT	900
	GTTTGAAACA	ATAGTTACAT	CTTGTGGCGT	CCGCAGCACA	AAAGACATAA	TCCGACTCTG	960
	TTTTGTAGGC	TATTTGAAGT	TTGGGATCAA	CACAGAAAAT	GACGCAACTG	TGTACCGGGA	1020
35	ATGGGCCCCCT	GCAGCAATGT	AAGTTCTAGT	GTTGTCACGC	AACTAATTGC	AATGGTCGTT	1080
	GGTTAACTTA	TGAAGTGCTG	ATGAAACTGT	CTTAAGAGTT	TATGGCTTGT	CTTTTCTGAT	1140
40	TCTAGCTAGT	AAAGAGTAGA	TAAATATGAA	ATATGTTTTT	CCTTTTCTAG	TTATGGTCAT	1200
	GGTTGGCTGG	TATTCATTTT	TTTTATGGCA	ATACTTGCTT	CTAACTATCT	TTAGTAGATT	1260
	CATGTATTTA	CTTGTGAGTC	ATTACTTTAT	GGGTGTAGGG	ATGCACAAC	TATTGGTGAC	1320
45	TTCAACAAC	GGAATGGCTC	TGGGCACAGG	ATGACAAAAG	ATAATTATGG	TGTTTGGTCA	1380
	ATCAGGATTT	CCCATGTCAA	TGGGAAACCT	GCCATCCCCC	ATAATTCCAA	GGTTAAATTT	1440
50	CGATTTACAC	GTGGAGATGG	ACTATGGGTC	GATCGGGTTC	CTGCATGGAT	TCGTTATGCA	1500
	ACTTTTGATG	CCTCTAAATT	TGGAGCTCCA	TATGACGGTG	TTCCTGGGA	TCCACCTTCT	1560
	GGTGAAAGGT	CTACTTTTAT	TGGCTCGAGA	GCAAGAAATC	TAAGTAAAC	CCACACAATT	1620
55	AACTTACATT	AATGTGGAGA	CATGATACTT	TTATTGCTCG	TTTTGCAGGT	ATGTGTTTAA	1680
	GCATCCTCGG	CCTCGAAAGC	CTGACGCTCC	ACGTATTTAC	GAGGCTCATG	TGGGGATGAG	1740
60	TGGTGAAAAG	CCTGAAGTAA	GCACATACAG	AGAATTTGCA	GACAATGTGT	TACCGCGCAT	1800
	AAAGGCAAAC	AACTACAACA	CAGTTCAGCT	GATGGCAATC	ATGGAACATT	CATATTATGC	1860
	TTCTTTTGGG	TACCATGTGA	CGAATTTCTT	CGCAGTTAGC	AGCAGATCAG	AACGCCAGAG	1920
65	ACCTCAATAT	CTTGTGACA	AGGCACATAG	TTTACGGTTG	CGTGTTCTGA	TGGATGTTGT	1980
	CCATAGCCAT	GCGAGCAGTA	ATAAGACAGA	TGGTCTTAAT	GGCTATGATG	TTGGGCAAAA	2040

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	ATGGACGAAT	TCATGTTTGA	TGGCTTCCGA	TTTGATGGGG	TAACATCCAT	GCTATATAAT	2220
	CACCATGGTA	TCAATATGTC	ATTCGCTGGA	AGTTACAAGG	AATATTTTGG	TTTGGATACT	2280
10	GATGTAGATG	CAGTTGTTTA	CCTGATGCTT	GCGAACCATT	TAATGCACAA	ACTCTTGCCA	2340
	GAAGCAACTG	TTGTTGCAGA	AGATGTTTCA	GGCATGCCAG	TGCTTTGTCTG	GTCAGTTGAT	2400
15	GAAGGTGGAG	TAGGGTTTGA	CTATCGCCTG	GCTATGGCTA	TTCTTGATAG	ATGGATCGAC	2460
	TACTTGAAGA	ACAAAGATGA	CCTTGAATGG	TCAATGAGTG	GAATAGCACA	TACTCTGACC	2520
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20	CCCTCCTTTG	TCGCTGTGCG	TGAGTATGTG	TTCTTTTTTT	ATGGGGCACT	GGTCTAAGAA	2640
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	GTATACTGGC	ATGTCAGACT	TGCAGCCTGC	TTCGCCTACA	ATTGATCGTG	GAATTGCACT	3000
35	TCAAAAGGTT	CGATTCGTTT	TAAGTATTCC	TGAATTTGAT	GTTCTAGTTC	CAGACGAGTA	3060
	TTGTAATGTT	CGTTGTTACT	CAGAGTTCCTG	CTTAGTCCTT	GAAGATAATG	TATTCCAGTC	3120
	CCTTTTG GTA	CATTG GCTT	ATTTTGTTAC	AAATATTTCA	GATGATTCAC	TTCATCACCA	3180
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	GTTTATATCT	GTTTCTAAC	TCATACTGAC	GGTGCAATTT	CCTTTTAGTT	TGGCCACCCA	3720
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60	TGGAGCCTCG	CAGACATTGA	TCACCTACGA	TACAAGGTTA	TGCCTATGTA	TATTTTTTACA	3840
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 5 CTGTGTTCTT TTGTTAACAG GAAGTTATTT TCTCTGCATC TGATAAATAA TAATAGCCTT 4200  
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 25 GACTTGCCCTG GGAAGTACAA GGTAGCTCTG GACTCTGATG CTCTGATGTT TGGTGGACAT 4800  
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 30 AGAAGGGGCC ATCAAGGCTG CATCAGATAA TCTTATTTGC AGTGTTGATC TGTGCTGCAT 4920  
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 35 TGGTAATGCT AATTACTAGG AGGATTTAGT AACAAATAAT AAATAACAGC AAAAGATATC 5100  
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 40 GGAAAAGCCC AAGGATGAAG GAGCTGCTTT CTTGGGGGAA ACTGCTCTCG GGTACATCGA 5220  
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 45 CAAAGACAAC AAATAAGCAC CATATCAACG CTTGATCAGG ACCGTGTGCC GACGTCCTTG 5400  
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 55 CATAGTTACA TGATAATTGA TGCATATTGC TATAAGCCTG GATTGCATCT TCTTTTGCTA 5700  
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GAACAGAAGC AACAGGGGCT TGGAAGTGA CGCCGAAAAT AAAGTCAAAC CGGCTGGGCC 6120  
 5 GGATTGAAAG GGGAAACGCC AAAATCCACT TAATTTGAAT GGAAGGAGGA ATGGTTCTTG 6180  
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## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 11463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE:

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: triticum tauschii  
 (F) TISSUE TYPE: Endosperm

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..11463  
 (D) OTHER INFORMATION: /product= "complete sequence of the  
 starch branching enzyme II gene"

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGAAACACCT CCATTTTAGA TTTTTTTTTT GTTCTTTTCG GACGGTGGGT CGTGGAGAGA 60  
 35 TTAGCGTCTA GTTTTCTTAA AAGAACAGGC CATTTAGGCC CTGCTTTACA AAAGGCTCAA 120  
 CCAGTCCAAA ACGTCTGCTA GGATCACCAG CTGCAAAGTT AAGCGCGAGA CCACCAAAAC 180  
 40 AGGCGCATTC GAACTGGACA GACGCTCAGC CAGGAGCCCA GCACCACAGG CTTGAGCCTG 240  
 ACAGCGGACG TGAGTGCCTG ACACATGGGG TCATCTATGG GCGTCGGAGC AAGGAAGAGA 300  
 GACGCACATG AACACCATGA TGATGCTATC AGGCCTGATG GAGGGAGCAA CCATGCACCT 360  
 45 TTTCCCTCTT GGAAATTCAT AGCTCACACT TTTTTTTAAT GGAAGCAAGA GTTGGCAAAC 420  
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 50 CCATGCACCG ACGAGTCCAT GCGAGGTGGA AACGAAGAAC TGAAAATCAA CATCCCAGTT 540  
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 55 TTTTACACG AAAATGCCAT AGCTGGCCCG CATGCGTGCA GATCGGATGA TCGGTCGGAG 720  
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 60 AAACAAAATA AATACTTATA AACGAGGGTA CTAGAGGCCG CTAACGGCAT GGCCAGGTAA 840  
 ACGCGCTCCC AGCCGTTGGT TTGCGATCTC GTCCTCCCGC ACGCAGCGTC GCCTCCACCG 900

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TCCGTCCGTC GCTGCCACCT CTGCTGTGCG CGCGCACGAA GGGAGGAAGA ACGAACGCCG 960  
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 5 CCTCTCCCCC GCCCATCCCC ATGCACTGCA CCGTACCCGC CAGCTTCCAC CCCC GCCGCA 1080  
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 10 TGCATTTTCGG CCGGCGGGTT GAGTGAGATC TGGGCGACTG GCTGACTCAA TCACTACGCG 1200  
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 15 AAGAAGGACT CCTCTCGTAC GCCTCGCTCT CTCGAATCTC CCCC GTCTGG CTTTGGCTCC 1380  
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 65 TAATTGCATA TCTTATAAGA AAATTTATAA TTCCTGTTTT CCCCTCTCTT TTTTCCAGTG 2880  
 CTGAAGGTAT CGTCTAATTG CATATCTTAT AAGAAAATTT ATATTCCTGT TTTCCCCTAT 2940

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	TTTCCAGTGC	TGAAGGTATC	ACTTACCGAG	AATGGGCTCC	CTGGAGCGCA	TGTTATGTTC	3000
5	TTTTAAGTTC	CTTAACGAGA	CACCTTCCAA	TTTATTGTTA	ATGGTCACTA	TTCACCAACT	3060
	AGCTTACTGG	ACTTACAAAT	TAGCTTACTG	AATACTGACC	AGTTACTATA	AATTTATGAT	3120
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	ATTATTAAAT	GAAATTTCCA	GTGTTACAGT	TTTTTAATAC	CCACTTCTTA	CTGACATGTG	3900
35	AGTCAAGACA	ATACTTTTGA	ATTTGGAAGT	GACATATGCA	TTAATTACAC	TTCTAAGGGC	3960
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	TCATTATTCT	GCGAGCGATT	CAAAAACCTC	CATTGTTCTG	AGGTGTACGT	ACTGCAGGGA	4680
60	TCTCCCATTA	TGAAGAGGAT	ATAGTTAATT	CTTTGTAACC	TACTTGGAAA	CTTGAGTCTT	4740
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 60 ACCTGATGAG ATCATGGAAG ATTGGAAGTG ATTATTATTT ATTTCTTTT TAAGTTTGTT 6720  
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	TAACAATGCT	AATTTATACC	TTGTATGATA	ATGCATCACT	TAGTAAATTTG	AAAAGTGCAG	7020
5	GGGCATTCAA	GCTTACGAGC	ATATTTTTTG	ATGGCTGTAA	TTTATTTGAT	AGTATGCTTG	7080
	TTTGGGTTTT	TCAATAAGTG	GGAGTGTGTG	ACTAATGTTG	TATTATTTAT	TTAATTGCGG	7140
	AAGAAATGGG	CAACCTTGTC	AATTGCTTCA	GAAGGCTAAC	TTTGATTTCA	TAAACGCTTT	7200
10	GGAAATGAGA	GGCTATTCCC	AAGGACATGA	ATTATACTTC	AGTGTGTTCT	GTACATGTAT	7260
	TTGTAATAGT	GGTTTAACTT	AAATTCCTGC	ACTGCTATGG	AATCTCACTG	TATGTTGTAG	7320
15	TGTACACATC	CACAAACAAG	TAATCCTGAG	CTTTCAACTC	ATGAGAAAAT	AGAGTCCGCT	7380
	TCTGCCAGCA	TTAACTGTTC	ACAGTTCTAA	TTTGTGTAAAC	TGTGAAATTG	TTCAGGTCAG	7440
	TGGAATGCCT	ACATTTTGCA	TCCCTGTTCC	AGATGGTGGT	GTTGGTTTTG	ACTACCGCCT	7500
20	GCATATGGCT	GTAGCAGATA	AATGGATTGA	ACTCCTCAAG	TAAGTGCAGG	AATATTGGTG	7560
	ATTACATGCG	CACAAATGATC	TAGATTACAT	TTTCTAAATG	GTA AAAAGGA	AAATATGTAT	7620
25	GTGAATATCT	AGACATTTGC	CTGTTATCAG	CTTGAATACG	AGAAGTCAAA	TACATGATTT	7680
	AAATAGCAAA	TCTCGGAAAT	GTAATGGCTA	GTGTCTTTAT	GCTGGGCAGT	GTACATTGCG	7740
	CTGTAGCAGG	CCAGTCAACA	CAGTTAGCAA	TATTTTCAGA	AACAATATTA	TTTATATCCG	7800
30	TATATGAGAA	AGTTAGTATA	TAACTGTGG	TCATTAATTG	TGTTACCTT	TTGTCCTGTT	7860
	TAAGGATGGG	CAGTAGGTAA	TAAATTTAGC	CAGATAAAAT	AAATCGTTAT	TAGGTTTACA	7920
35	AAAGGAATAT	ACAGGGTCAT	GTAGCATATC	TAGTTGTAAT	TAATGAAAAG	GCTGACAAAA	7980
	GGCTCGGTAA	AAAAAATTT	ATGATGATCC	AGATAGATAT	GCAGGAACGC	GACTAAAGCT	8040
	CAAATACTTA	TTGCTACTAC	ACAGCTGCCA	ATCTGTCATG	ATCTGTGTTT	TGCTTTGTGC	8100
40	TATTTAGATT	TAAATACTAA	CTCGATACAT	TGGCAATAAT	AACTTAACCT	ATTCAACCAA	8160
	TTTGGTGGAT	ACCAGAAATTT	CTGCCCTCTT	GTTAGTAATG	ATGTGCTCCC	TGCTGCTGTT	8220
45	CTCTGCCGTT	ACAAAAGCTG	TTTTCAGTTT	TTTGCATCAT	TATTTTTGTG	TGTGAGTAGT	8280
	TTAAGCATGT	TTTTTGAAGC	TGTGAGCTGT	TGGTACTTAA	TACATTCTTG	GAAGGTCCCA	8340
	AATATGCTGC	AGTGTAATTT	AGCATTCTCT	TAACACAGGC	AAAGTGACGA	ATCTTGGAAG	8400
50	ATGGGCGATA	TTGTGCACAC	CCTAACAAAT	AGAAGGTGGC	TTGAGAAGTG	TGTAACCTAT	8460
	GCAGAAAGTC	ATGATCAAGC	ACTAGTTGGT	GACAAGACTA	TTGCATTCTG	GTTGATGGAT	8520
55	AAGGTACTAG	CTGTTACTTT	TGGACAAAAG	AATTACTCCC	TCCCGTTCCT	AAATATAAGT	8580
	CTTTGTAGAG	ATTCCACTAT	GGACCACATA	GTATATAGAT	GCATTTTAGA	GTGTAGATTCT	8640
	ACTCATTTTG	CTTCGTATGT	AGTCCATAGT	GAAATCTCTA	CAGAGACTTA	TATTTAGGAA	8700
60	CGGAGGGAGT	ACATAATTGA	TTTGTCTCAT	CAGATTGCTA	GTGTTTTCTT	GTGATAAAGA	8760
	TTGGCTGCCT	CACCCATCAC	CAGCTATTTT	CCAAGTGTTA	CTTGAGCAGA	ATTTGCTGAA	8820
65	AACGTACCAT	GTGGTACTGT	GGCGGCTTGT	GAACCTTGAC	AGTTATGTTG	CAATTTTCTG	8880
	TTCTTATTTA	TTTGATTGCT	TATGTTACCG	TTCATTTGCT	CATTCCTTTT	CGAGACCAGC	8940

	CAAAGTCACG	TGTTAGCTGT	GTGATCTGTT	ATCTGAATCT	TGAGCAAATT	TTATTAATAG	9000
	GCTAAAATCC	AACGAATTAT	TTGCTTGAAT	TTAAATATAC	AGACGTATAG	TCACCTGGCT	9060
5	CTTCTCTAGA	TGATTACCAT	AGTGCCTGAA	GGCTGAAATA	GTTTTGGTGT	TTCTTGGATG	9120
	CCGCCTAAAG	GAGTGATTTT	TATTGGATAG	ATTCCTGGCC	GAGTCTTCGT	TACAACATAA	9180
10	CATTTTGGAG	ATATGCTTAG	TAACAGCTCT	GGGAAGTTTG	GTCACAAGTC	TGCATCTACA	9240
	CGCTCCTTGA	GGTTTTATTA	TGGCGCCATC	TTTGTAACTA	GTGGCACCTG	TAAGGAAACA	9300
	CATTCAAAAG	GAAACGGTCA	CATCATTCTA	ATCAGGACCA	CCATACTAAG	AGCAAGATTC	9360
15	TGTTCCAATT	TTATGAGTTT	TTGGGACTCC	AAAGGGAACA	AAAGTGCTCT	ATATTGTGCT	9420
	TATAACTACA	GTTGTTTTTA	TACCAGTGTA	GTTTTATTCC	AGGACAGTTG	ATACTTGGTA	9480
20	CTGTGCTGTA	AATTATTTAT	CCGACATAGA	ACAGCATGAA	CATATCAAGC	TCTCTTTGTG	9540
	CAGGATATGT	ATGATTTTCAT	GGCTCTGGAT	AGGCTTCAAC	TCTTCGCATT	GATCGTGGCA	9600
	TAGCATTACA	TAAAATGATC	AGGCTTGTC	CCATGGGTTT	AGGTGGTGAA	GGCTATCTTA	9660
25	ACTTCATGGG	AAATGAGTTT	GGGCATCCTG	GTCAGTCTTT	ACAACATTAT	TGCATTCTGC	9720
	ATGATTGTGA	TTTACTGTAA	TTTGAACCAT	GCTTTTCTTT	CACATTGTAT	GTATTATGTA	9780
30	ATCTGTTGCT	TCCAAGGAGG	AAGTTAACTT	CTATTTACTT	GGCAGAATGG	ATAGATTTTC	9840
	CAAGAGGCC	ACAAACTCTT	CCAACCGGCA	AAGTTCCTCC	CTGGAAATAA	CAATAGTTAT	9900
	GATAAATGCC	GCCGTAGATT	TGATCTTGTA	AGTTTTAGCT	GTGCTATTAC	ATTCCCTCAC	9960
35	TAGATCTTTA	TTGGCCATTT	ATTTCTTGAT	GAAATCATAA	TGTTTGTTAG	GAAAGATCAA	10020
	CATTGCTTTT	GTAGTTTTGT	AGACGTTAAC	ATAAGTATGT	GTTGAGAGTT	GTTGATCATT	10080
40	AAAAATATCA	TGATTTTTTG	CAGGGAGATG	CAGATTTTCT	TAGATATCGT	GGTATGCAAG	10140
	AGTTCGATCA	GGCAATGCAG	CATCTTGAGG	AAAAATATGG	GGTATGTCAC	TGGTTTGTCT	10200
	TTGTTGCATA	ACAAGTCACA	GTTTAACGTC	AGTCTCTTCA	AGTGGTAAAA	AAAGTGTAAG	10260
45	ATTAATTCCT	GTAATGAGAT	GAAAACTGTG	CAAAGGCGGA	GCTGGAATTG	CTTTTCACCA	10320
	AAACTATTTT	CTTAAGTGCT	TGTGTATTGA	TACATATACC	AGCACTGACA	ATGTAACGTC	10380
50	AGTTTATGAC	ATCTGAGCAC	CAGTATGTTT	CACGGAAACA	TGAGGAAGAT	AAGGTGATCA	10440
	TCCTCAAAAG	AGGAGATTTG	GTATTTGTTT	TCAACTTCCA	CTGGAGCAAT	AGCTTTTTTG	10500
	ACTACCGTGT	TGGGTGTTCC	AAGCCTGGGA	AGTACAAGGT	ATGCTTGCCT	TTTCATTGTC	10560
55	CACCCTTCAC	CAGTAGGGTT	AGTGGGGGCT	TCTACAACCT	TTAATTCCAC	ATGGATAGAG	10620
	TTTGTTGGTC	GTGCAGCTAT	CAATATAAAG	AATAGGGTAA	TTTGTAAGA	AAAGAATTTG	10680
60	CTCGAGCTGT	TGTAGCCATA	GGAAGGTTGT	TCTTAACAGC	CCCGAAGCAC	ATACCATTCA	10740
	TTCATATTAT	CTACTTAAGT	GTTTGTTTCA	ATCTTTATGC	TCAGTTGGAC	TCGGTCTAAT	10800
	ACTAGAATA	TTTTCCGAAT	CTACCCTAAC	CATCCTAGCA	GTTTTAGAGC	AGCCCCATTT	10860
65	GGACAATTGG	CTGGGTTTTT	GTTAGTTGTG	ACAGTTTCTG	CTATTTCTTA	ATCAGGTGGC	10920
	CTTGGAATCT	GACGATGCAC	TCTTTGGTGG	ATTCAGCAGG	CTTGATCATG	ATGTCGACTA	10980

45	TCTCCCACTC	TTTCTCTCCCC	GCGCACACCG	AGTCGGCACC	GGCTCATCAC	CCATCACCTC	60
	GGCCTCGGCC	ACCGGCAAAC	CCCCCGATCC	GCTTTTGCAG	GCAGCGCACT	AAAACCCCGG	120
	GGAGCGCGCC	CCGCGGCAGC	AGCAGCACCG	CAGTGGGAGA	GAGAGGCTTC	GCCCCGGCCC	180
50	GCACCGAGCG	GGGCGATCCA	CCGTCCGTGC	GTCCGCACCT	CCTCCGCCTC	CTCCCTGTCT	240
	CCGCGCGCCC	ACACCCATGG	CGGCGACGGG	CGTCGGCGCC	GGGTGCCTCG	CCCCAGCGT	300
	CCGCC'TGCGC	GCCGATCCGG	CGACGGCGGC	CCGGGCGTCC	GCCTGCGTCG	TCCGCGCGCG	360
55	GCTCCGGCGC	TTGGCGCGGG	GCCGCTACGT	TGCCGAGCTC	AGCAGGGAGG	GCCCCGCGGC	420
	GCGCCCCGCG	CAGCAGCAGC	AACTGGCCCC	GCCGCTCGTG	CCAGGCTTCC	TCGCGCCGCC	480
	60	GCCGCCCCGCG	CCCGCCCAGT	CGCCGGCCCC	GACGCAGCCG	CCCCTGCCGG	ACGCCGGCGT
GGGGGAACTC		GCGCCCCGACC	TCCTGCTCGA	AGGGATTGCT	GAGGATTCCA	TCGACAGCAT	600

GGGGGAAGCTC GCGCCCGACC TCCTGCTCGA AGGGATTGCT GAGGATTCCA TCGACAGCAT 600

	AATTGTGGCT	GCAAGTGAGC	AGGATTCTGA	GATCATGGAT	GCGAATGAGC	AACCTCAAGC	650
5	TAAAGTTACA	CGTAGCATCG	TGTTTGTGAC	TGGTGAAGCT	GCTCCTTATG	CAAAGTCAGG	720
	GGGGCTGGGA	GATGTTTGTG	GTTTCGTTACC	AATTGCTCTT	GCTGCTCGTG	GTCACCGTGT	780
	GATGGTTGTA	ATGCCAAGAT	ACTTGAATGG	GTCCTCTGAT	AAAAACTATG	CAAAGGCATT	840
10	ATACACTGGG	AAGCACATTA	AGATTCCATG	CTTTGGGGGA	TCACATGAAG	TGACCTTTTTT	900
	TCATGAGTAT	AGAGACAACG	TCGATTGGGT	GTTTGTGCGAT	CATCCGTCAT	ATCATAGACC	960
15	AGGAAGTTTA	TATGGAGATA	ATTTTGGTGC	TTTGTGGTGAT	AATCAGTTCA	GATACACACT	1020
	CCTTTGCTAT	GCTGCATGCG	AGGCCCCACT	AATCCTTGAA	TTGGGAGGAT	ATATTTATGG	1080
	ACAGAATTGC	ATGTTTGTTG	TGAACGATTG	GCATGCCAGC	CTTGTGCCAG	TCCTTCTTGC	1140
20	TGCAAAATAT	AGACCATACG	GTGTTTACAG	AGATTCCCGC	AGCACCCCTG	TTATACATAA	1200
	TTTAGCACAT	CAGGGTCTGG	AGCCTGCAAG	TACATATCCT	GATCTGGGAT	TGCCACCTGA	1260
25	ATGGTATGGA	GCTTTAGAAT	GGGTATTTCC	AGAATGGGCA	AGGAGGCATG	CCCTTGACAA	1320
	GGGTGAGGCA	GTTAACTTTT	TGAAAGGAGC	AGTCGTGACA	GCAGATCGAA	TTGTGACCGT	1380
	CAGTCAGGGT	TATTCATGGG	AGGTCACAAC	TGCTGAAGGT	GGACAGGGCC	TCAATGAGCT	1440
30	CTTAAGCTCC	CGAAAAAGTG	TATTGAATGG	AATTGTAAAT	GGAATTGACA	TTAATGATTG	1500
	GAACCCACC	ACAGACAAGT	GTCTCCCTCA	TCATTATTCT	GTCGATGACC	TCTCTGGA	1560
35	GGCCAAATGT	AAAGCTGAAT	TGCAGAAGGA	GCTGGGTTTA	CCTGTAAGGG	AGGATGTTCC	1620
	TCTGATTGGC	TTTATTGGAA	GACTGGATTA	CCAGAAAGGC	ATTGATCTCA	TTAAATGGC	1680
	CATTCCAGAG	CTCATGAGGG	AGGACGTGCA	GTTTGTGATG	CTTGGATCTG	GGGATCCAAT	1740
40	TTTTGAAGGC	TGGATGAGAT	CTACCGAGTC	GAGTTACAAG	GATAAATTCC	GTGGATGGGT	1800
	TGGATTTAGT	GTTCCAGTTT	CCCACAGAAT	AACTGCAGGT	TGCGATATAT	TGTTAATGCC	1860
45	ATCCAGGTTT	GAACCTTG TG	GTCTTAATCA	GCTATATGCT	ATGCAATATG	GTACAGTTCC	1920
	TGTAGTTCAT	GGAAC TGGG	GCCTCCGAGA	CACAGTCGAG	ACCTTCAACC	CTTTTGGTGC	1980
	AAAAGGAGAG	GAGGGTACAG	GGTGGGCGTT	CTCACCGCTA	ACCGTGGACA	AGATGTTGTG	2040
50	GGCATTGCGA	ACCGCGATGT	CGACATTCAG	GGAGCACAAG	CCGTCC TGGG	AGGGGCTCAT	2100
	GAAGCGAGGC	ATGACGAAAG	ACCATACGTG	GGACCATGCC	GCCGAGCAGT	ACGAGCAGAT	2160
55	CTTCGAATGG	GCCTTCGTGG	ACCAACCCTA	CGTCATGTAG	ACGGGGACTG	GGGAGGTCGA	2220
	AGCGCGGGTC	TCCTTGAGCT	CTGAAGACAT	GTTCTCATC	CTTCCGCGGC	CCGGAAGGAT	2280
	ACCCCTGTAC	ATTGCGTTGT	CCTGCTACAG	TAGAGTCGCA	ATGCGCCTGC	TTGCTTGGTC	2340
60	CGCCGGTTTCG	AGAGTAGATG	ACGGCTGTGC	TGCTGCGGCG	GTGACAGCTT	CGGGTGGATG	2400
	ACAGTTACAG	TTTTGGGGAA	TAAGGAAGGG	ATGTGCTGCA	GGATGGTTAA	CAGCAAAGCA	2460
65	CCACTCAGAT	GGCAGCCTCT	CTGTCCGTGT	TACAGCTGAA	ATCAGAAACC	AACTGGTGAC	2520
	TCTTTAGCCT	TAGCGATTGT	GAAGTTTGTT	GCATTCTGTG	TATGTTGTCT	TGTCCTTAGC	2580

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TGACAAATAT TAGACCTGTT GGAGAATTTT ATTTATCTTT GCTGCTGTTG TTTTGTGTTT 2640  
 GTTAAAAAAA AAAAAAAAAA AA 2662

## 5 (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 10 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: NO

15

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: triticum tauschii

## (ix) FEATURE:

- 20 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..768

## (ix) FEATURE:

- 25 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..768  
 (D) OTHER INFORMATION: /product= "deduced amino acid  
 sequence SBE II"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

30

Met Ala Thr Phe Ala Val Ser Gly Ala Thr Leu Gly Val Ala Arg Pro  
 1 5 10 15

35

Pro Ala Ala Ala Gln Pro Glu Glu Leu Gln Ile Pro Glu Asp Ile Glu  
 20 25 30

Glu Gln Thr Ala Glu Val Asn Met Thr Gly Gly Thr Ala Glu Lys Leu  
 35 40 45

40

Glu Ser Ser Glu Pro Thr Gln Gly Ile Val Glu Thr Ile Thr Asp Gly  
 50 55 60

45

Val Thr Lys Gly Val Lys Glu Leu Val Val Gly Glu Lys Pro Arg Val  
 65 70 75 80

Val Pro Lys Pro Gly Asp Gly Gln Lys Ile Tyr Glu Ile Asp Pro Thr  
 85 90 95

50

Leu Lys Asp Phe Arg Ser His Leu Asp Tyr Arg Tyr Ser Glu Tyr Arg  
 100 105 110

Arg Ile Arg Ala Ala Ile Asp Gln His Glu Gly Gly Leu Glu Ala Phe  
 115 120 125

55

Ser Arg Gly Tyr Glu Lys Leu Gly Phe Thr Arg Ser Ala Glu Gly Ile  
 130 135 140

Thr Tyr Arg Glu Trp Ala Pro Gly Ala His Ser Ala Ala Leu Val Gly  
 145 150 155 160

60

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[illegible]



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Ala Val Ala Asp Lys Trp Ile Glu Leu Leu Lys Gln Ser Asp Glu Ser  
500 505 510

5 Trp Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu  
515 520 525

Glu Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly  
530 535 540

10 Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe  
545 550 555 560

Met Ala Leu Asp Arg Pro Ser Thr Pro Arg Ile Asp Arg Gly Ile Ala  
565 570 575

15 Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu Gly Gly Glu Gly  
580 585 590

20 Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp  
595 600 605

Phe Pro Arg Gly Pro Gln Thr Leu Pro Thr Gly Lys Val Leu Pro Gly  
610 615 620

25 Asn Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp  
625 630 635 640

Ala Asp Phe Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met  
645 650 655

30 Gln His Leu Glu Glu Lys Tyr Gly Phe Met Thr Ser Glu His Gln Tyr  
660 665 670

35 Val Ser Arg Lys His Glu Glu Asp Lys Val Ile Ile Phe Glu Arg Gly  
675 680 685

Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn Ser Phe Phe Asp  
690 695 700

40 Tyr Arg Val Gly Cys Ser Arg Pro Gly Lys Tyr Lys Val Ala Leu Asp  
705 710 715 720

Ser Asp Asp Ala Leu Phe Gly Gly Phe Ser Arg Leu Asp His Asp Val  
725 730 735

45 Asp Tyr Phe Thr Thr Glu His Pro His Asp Asn Arg Pro Arg Ser Phe  
740 745 750

50 Ser Val Tyr Thr Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Thr Glu  
755 760 765

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10550 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(A) ORGANISM: *triticum tauschii*

5 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:1..316  
(D) OTHER INFORMATION:/product= "exon 1"

10 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:1472..1828  
(D) OTHER INFORMATION:/product= "exon 2"

15 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:2766..2823  
(D) OTHER INFORMATION:/product= "exon 3"

20 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:2906..3028  
(D) OTHER INFORMATION:/product= "exon 4"

25 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:4113..4194  
(D) OTHER INFORMATION:/product= "exon 5"

30 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:4286..4459  
(D) OTHER INFORMATION:/product= "exon 6"

35 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:4562..4643  
(D) OTHER INFORMATION:/product= "exon 7"

40 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:4744..4855  
(D) OTHER INFORMATION:/product= "exon 8"

45 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:4999..5021  
(D) OTHER INFORMATION:/product= "exon 9"

50 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:5102..5192  
(D) OTHER INFORMATION:/product= "exon 10"

55 (ix) FEATURE:  
(A) NAME/KEY: exon  
(B) LOCATION:8593..8718

(D) OTHER INFORMATION:/product= "exon 11"

(ix) FEATURE:

(A) NAME/KEY: exon

5 (B) LOCATION:8807..8915

(D) OTHER INFORMATION:/product= "exon 12"

(ix) FEATURE:

(A) NAME/KEY: exon

10 (B) LOCATION:8992..9104

(D) OTHER INFORMATION:/product= "exon 13"

(ix) FEATURE:

(A) NAME/KEY: exon

15 (B) LOCATION:9161..9199

(D) OTHER INFORMATION:/product= "exon 14"

(ix) FEATURE:

(A) NAME/KEY: exon

20 (B) LOCATION:9498..9713

(D) OTHER INFORMATION:/product= "exon 15"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

25	ATGGCGGCGA CGGGCGTCCG CGCCGGGTGC CTCGCCCCCA GCGTCCGCCT	50
	GCGCGCCGAT CCGGCGACGG CGGCCCGGGC GTCCGCTTGC GTCGTCCGCG	100
	CGCGGCTCCG GCGCTTGGCG CGGGGCCGCT ACGTCGCCGA GCTCAGCAGG	150
30	GAGGGCCCCG CGGCGCGCCC CGCGCAGCAG CAGCAACTGG CCCC GCCGCT	200
	CGTGCCAGGC TTCCTCGCGC CGCCGCCGCC CGCGCCCGCC CAGTCGCCGG	250
35	CCCCGACGCA GCCGCCCTG CCGGACGCCG GCGTGGGGGA ACTCGCGCCC	300
	GACCTCCTGC TCGAAGGTAA AAAACAAGGC TGAATCCTCA GATCACTCCG	350
	CGTCTTCGTT TTACCAAATA CGGTACTGCG AAGTGGTGCT GTATATGTGA	400
40	AGTTTCTGTC GATTTCTTCC TGACGGATGT TCAGTCGATT CAGTTGTATA	450
	TATGTGATAC GTTCGTTGTT CATCGATCGT ACAGATTTAC CAGCACACTA	500
45	GATAGAAATC GAGACCGACG CGGGCAGATC AATAGATTTT TCTAGACGTT	550
	TTATTGGATC GTGAGATGAT TGATTGGGGT GCGTGTCGA TACGATAGCG	600
	GTGCACCGCC GATGTATCGG GGCATGTGCA CGTGGTTGGG TCTCAGCAGA	650
50	CATATCACTA GACTGGTATC GTAATTTACT AGTACTACTG GAAAGAGGAC	700
	TAAAAAGGCT AGGCCAAGTG CACGCATGTT GGAACGTTG TTAAATTGAT	750
55	GAGTTTGTCC TTTGCTTGGG CTGGTATTAT TACCAAAAAA TGGTGTTAGT	800

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	CCCTGTACTT ATTAATGGGA AAATCTTAAC ATGACACTGG GGTTTATGAG	850
	TCTCCAATTG TATATTCTCA GCACTCAACT GATTTTACTG ATACTGTAGT	900
5	GGAAATGACA CGTGAGCACC CCCCTTCAAG GAATGCAATG CTTCTTTCTG	950
	TTTTATATTA CAGGAAGTAG AAGGAGCTTC CACCTTTGAG TACAGAAGTA	1000
	CTCCCTCCGT TCCAAAATAG ATGACTCAAC TTTGTACTAA TTTTGTACTA	1050
10	TAGTTAGTAC AAAGTTGAGT CATCTATTTT AGAACGGAGG GAGTAGTATC	1100
	GAAATTGAAG ACCCTTGTAT TACTGTCTTG TTTTCAATG AAAATGGGAG	1150
15	GCCCATGCAG TAAGTCACAT GGGCACCTGG GAGGCTGGGA TCATGTGTGC	1200
	TTTGCAGAGT ACTAGACCCA GCTCACCTC TGTTAGATTA CTTGTTGGGC	1250
	TGCTACTTTG TGTTTGCTGT GCAGTATATC AGACATCCTG AATTTGGCAT	1300
20	CTAGCTGAGA ACAGAATGCA GGTTCACCA TTCTTATTAT TGCTAAACTG	1350
	TTGTCACGCA ATTTATAAAG AATGTGATCT TCTGAGTATT AATTAATCAT	1400
25	GTTCTGCTAA TATCTGTCCT CGCTCTGGTG TTGACAAATA TACCATATGA	1450
	ATATTTTCCA TTTTGCAACC AGGGATTGCT GAGGATTCCA TCGACAGCAT	1500
	AATCGTGGCT GCAAGTGAGC AGGATTCTGA GATCATGGAT GCGAATGAGC	1550
30	AACCTCAAGC TAAAGTTACA CGTAGCATCG TGTTTGTGAC TGGTGAAGCT	1600
	GCTCCTTATG CAAAGTCAGG GGGGCTGGGA GATGTTTGTG GTTCGTTACC	1650
35	AATTGCTCTT GCTGCTCGTG GTCACCGTGT GATGGTTGTA ATGCCAAGAT	1700
	ACTTGAATGG GTCCTCTGAT AAAAATATG CAAAGGCATT ATACACTGCG	1750
	AAGCACATTA AGATTCCATG CTTTGGGGGA TCACATGAAG TGACCTTTTT	1800
40	TCATGAGTAT AGAGACAACG TCGATTGGGT GGTACACAA TCACCTTCTT	1850
	ATTCTCTGTT GAATTGTAGC AACTGTTTAT CCTTGTTTAC ACTTCTTTTA	1900
45	GCCCTGCAAA GACATATGTG ATTTCCATAC TTTTTGTTA TTTCCCTTGT	1950
	ACTCTTGCTC ATGAAGGTCA AAATATCATA TATCCATGGA AGTCATGCAT	2000
	GTGCCTAGTA TTTTGGTGT CGGTGCCTTT AACTTTCAGG GATTAATACG	2050
50	TGGAATTTGA TAACTAAAGT TTATTTTATT GAAAAAATT GTAGGTTGG	2100
	TGAGCCCACA GCCACGCAGT GGCACCACTG CTTGCACATG ATTTTGCATT	2150
55	TCTGTTTGCA CCGAGCACTT CATGTGAATA AGGTGTAAAA TCATAAAGTA	2200

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	CCAATTTTAT TCTGCCAATT GCACTTAAGA GTATATACAT TTATCTTGGC	2250
	CTCAATCATG GGAGTACTGT GCATTCAGTG CACCATCATT GTTCTAAGGA	2300
5	GAAAATGTGG GTGCAAGGAA GACACTTTTG TCCCTTAATA AAAGGCAGGC	2350
	ACTCTGTTGT CATATAGATA GAAAGCAACA AACTTATTTT AAAGAGCTAA	2400
10	CAATGGCAAA AGAACCACAAA AAAGCATGCT AAGGCGGTGA CACCAAAAGG	2450
	TGAGGGGGGC CTTGTGACTG ACAGCACCCC AAACCTATTGC CATTGTTTTA	2500
	CTAAATGAAG ATCATTTTAG AAGCTCTCAG GAACTTCGAA AACAGTGGCT	2550
15	TTCCGTCCAC AGATCGTCTG TTAATATTTT TGTCCAGTGA TACTTTTTTT	2600
	GCTCCTTACA AGAGTGCCTA TGTTGACATA TACATTGTTA AGTTGTTTAT	2650
20	AAGTTTACTT CTTATTCTAA ACAGCAAGTG CCTAATGCTT GCATTTATTT	2700
	TGGCTATTTA TTTTATTCT CATTTCATC AACACTTTTG TTCAGGTGTT	2750
	TGTCGATCAT CCGTCATATC ATAGACCAGG AAGTTTATAT GGAGATAATT	2800
25	TTGGTGCTTT TGGTGATAAT CAGGTACACT AACTATACT AAGCTCCTAG	2850
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35	AAAGTCCAAT CCTTTATTCA TTCTCTGCTT TGCAGTGTGC CCATGTCTAC	3100
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40	TGGAGTCTAA AAGTTACCGG AGGGAATAAC TCTTAAGGAT TTCCTCAATC	3200
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15	GCTGGCTTAT TTTGTACAAG TATCGATGTT AGATGCATAT TTCCTTTTGT	4000
	TCTTG TGCTG TTTGCCATGT TGTATTCCCC TTTTCTGTCG CCAGTGTTGC	4050
20	ATGTTAAATT GGTTTTCAAT ACATAATCAA CTTTGTTGCT GACATCAGTC	4100
	ATTTTTATT CAGCCTTCTTG CTGCAAATA TAGACCATAC GGTGTTTACA	4150
	GAGATTCCCG CAGCACCTT GTTATACATA ATTTAGCACA TCAGGTTTGG	4200
25	GTCTATCACC TTTCATTATC CGTACATGGC TTTGTAAGTC GGTTACACCG	4250
	TATCGTCATA CTGTATGTTA TTTCAATGTC ATTAGGGTGT GGAGCCTGCA	4300
30	AGTACATATC CTGATCTGGG ATTGCCACCT GAATGGTATG GAGCTTTAGA	4350
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	CTTCAGTTCA ATTGCCCTGT CTTTCACCCA ATTAAGAAAT GATTTAATCT	4550
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	GGGAGTACTT CGACAAGCTG TTCAATGGGG AGGATGAGAG TCCTACCATT	7350
	GAACTTGACG ACTCCTTTGA TGAGACCATC ATGCGTTTTA TGCGGCGAAT	7400
	CCAGGAGTCC GAGGTCAAGG AGGCTTTAAA AAGGAGGCAA GGCGATGGGC	7450
	CCTGATTGTA TCCCCATTGA GGTGTGGAAA GGCCTCGGGG ACATAGCGAT	7500
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	CGAGTACATG ATGTGCGGTT TCAGTACTAC TAGGTGTGAG GAGGAGGAGG	8250

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	TTAGCCTTGA TGGGCAGGTG GTACCCCA AGGACACCTT TCGATATTTG	8300
	GGGTCAATGC TGCAGGAGGA TGGGGGTATT GATGAAGATG TGAACCATCG	8350
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5	ACCCGCAATG TTGTATGGCG CTGAGTGTTG GCCGACTAAA AGGCGACATG	8500
	TTCAACAGTT AGGTGTGGCG GAGATGCGTA TGTTGAGATG GATGTGTGGC	8550
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(2) INFORMATION FOR SEQ ID NO: 14:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 647 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(A) ORGANISM: triticum tauschii  
(F) TISSUE TYPE: Endosperm

(A) NAME/KEY: Protein  
(B) LOCATION: 1..647  
(D) OTHER INFORMATION: /product= "deduced amino acid sequence for SSS I"

15	Met 1	Ala	Ala	Thr		Gly 5	Val	Gly	Ala	Gly	Cys 10	Leu	Ala	Pro	Ser	Val	Arg 15
	Leu	Arg	Ala	Asp 20	Pro	Ala	Thr	Ala	Ala 25	Arg	Ala	Ser	Ala	Cys 30	Val	Val	
20	Arg	Ala	Arg 35	Leu	Arg	Arg	Leu	Ala 40	Arg	Gly	Arg	Tyr	Val 45	Ala	Glu	Leu	
	Ser	Arg 50	Glu	Gly	Pro	Ala	Ala 55	Arg	Pro	Ala	Gln	Gln 60	Gln	Gln	Leu	Ala	
25	Pro 65	Pro	Leu	Val	Pro	Gly 70	Phe	Leu	Ala	Pro	Pro 75	Pro	Pro	Ala	Pro	Ala 80	
	Gln	Ser	Pro	Ala	Pro 85	Thr	Gln	Pro	Pro	Leu 90	Pro	Asp	Ala	Gly	Val 95	Gly	
30	Glu	Leu	Ala	Pro 100	Asp	Leu	Leu	Leu	Glu 105	Gly	Ile	Ala	Glu	Asp 110	Ser	Ile	
	Asp	Ser	Ile 115	Ile	Val	Ala	Ala	Ser 120	Glu	Gln	Asp	Ser	Glu 125	Ile	Met	Asp	
35	Ala	Asn 130	Glu	Gln	Pro	Gln	Ala 135	Lys	Val	Thr	Arg	Ser 140	Ile	Val	Phe	Val	
40	Thr 145	Gly	Glu	Ala	Ala	Pro 150	Tyr	Ala	Lys	Ser	Gly 155	Gly	Leu	Gly	Asp	Val 160	
	Cys	Gly	Ser	Leu	Pro 165	Ile	Ala	Leu	Ala	Ala 170	Arg	Gly	His	Arg	Val 175	Met	
45	Val	Val	Met	Pro 180	Arg	Tyr	Leu	Asn	Gly 185	Ser	Ser	Asp	Lys	Asn 190	Tyr	Ala	
	Lys	Ala 195	Leu	Tyr	Thr	Gly	Lys	His 200	Ile	Lys	Ile	Pro	Cys 205	Phe	Gly	Gly	
50	Ser 210	His	Glu	Val	Thr	Phe	Phe 215	His	Glu	Tyr	Arg	Asp 220	Asn	Val	Asp	Trp	
55	Val 225	Phe	Val	Asp	His	Pro 230	Ser	Tyr	His	Arg	Pro 235	Gly	Ser	Leu	Tyr	Gly 240	
	Asp	Asn	Phe	Gly	Ala 245	Phe	Gly	Asp	Asn	Gln 250	Phe	Arg	Tyr	Thr	Leu 255	Leu	
60	Cys	Tyr	Ala	Ala 260	Cys	Glu	Ala	Pro	Leu 265	Ile	Leu	Glu	Leu	Gly 270	Gly	Tyr	

Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His Ala Ser  
 275 280 285  
 5 Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr  
 290 295 300  
 Arg Asp Ser Arg Ser Thr Leu Val Ile His Asn Leu Ala His Gln Gly  
 305 310 315 320  
 10 Leu Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp  
 325 330 335  
 Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala  
 340 345 350  
 15 Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr  
 355 360 365  
 Ala Asp Arg Ile Val Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr  
 370 375 380  
 20 Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser Arg Lys  
 385 390 395 400  
 25 Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn  
 405 410 415  
 Pro Thr Thr Asp Lys Cys Leu Pro His His Tyr Ser Val Asp Asp Leu  
 420 425 430  
 Ser Gly Lys Ala Lys Cys Lys Ala Glu Leu Gln Lys Glu Leu Gly Leu  
 435 440 445  
 35 Pro Val Arg Glu Asp Val Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp  
 450 455 460  
 Tyr Gln Lys Gly Ile Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met  
 465 470 475 480  
 40 Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe  
 485 490 495  
 Glu Gly Trp Met Arg Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg  
 500 505 510  
 45 Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr Ala Gly  
 515 520 525  
 Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn  
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 545 550 555 560  
 55 Gly Gly Leu Arg Asp Thr Val Glu Thr Phe Asn Pro Phe Gly Ala Lys  
 565 570 575  
 Gly Glu Glu Gly Thr Gly Trp Ala Phe Ser Pro Leu Thr Val Asp Lys  
 580 585 590  
 60 Met Leu Trp Ala Leu Arg Thr Ala Met Ser Thr Phe Arg Glu His Lys  
 595 600 605

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Pro Ser Trp Glu Gly Leu Met Lys Arg Gly Met Thr Lys Asp His Thr  
 610 615 620

5 Trp Asp His Ala Ala Glu Gln Tyr Glu Gln Ile Phe Glu Trp Ala Phe  
 625 630 635 640

Val Asp Gln Pro Tyr Val Met  
 645

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(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5072 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: triticum tauschii

(F) TISSUE TYPE: Endosperm

25 (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 1..4993

(D) OTHER INFORMATION: /function= "region containing promoter of SSS I"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCTAGATGCA TGCTGGATAG CGGTCGATGT GTGGAGTAAT AGTAGTAGAT GCAGAATCGT 60

35 TTCGGTCTAC TTGTCGCGGA CGTGATGCCT ATATACATGA TCATACCTAG ATATTCTCAT 120

AACATGCTC AATTCTATCA ATTGCTCGAC AGTAATTCGT TTACCCACCG TAATACTTAT 180

40 GATCTTGAGA GAAGTCACTA GTGAAACCTA TGCCCCCAG GTCTATTTTG CATCATATTA 240

ATCTTCCAAT ACTTAGTTAT TTCCATTGCC GTTTATTTTA CTTTGTATCT TTATTCTTTT 300

TTATTATAAA AAATACCAA AATATTATCT TATCATATCT ATCAGATCTC ATTCTCGTAA 360

45 GTGACCGTGA AGGGATTGAC AACCCCTTTA TCGTGTGGT TCGGAGGTTT TTGTTTGT 420

GTGTAGGTGC GTGTGACTCG CACGTCTCCT ACTGGATTGA TACCTGGGT TTTCAAAAAC 480

TGAGAAAAAT ACTTACGCTA CTTTACTGCA TAACCCTTTC CTCTTTAAAA AAAAAACCA 540

50 ACGTAGTATT CAAGAGGTAG CACGCTACCA TCCTCTCCAA CAGGAGCGCG GAGATCTTTG 600

TCCGGCAGGT TGATGCGGGC CGGGGAAGAA CTCCAGCTGC CTTGGCCAGC TTGGTCGTGA 660

55 GCCGCCCCAG CGGCGTCTTG AACCTGTCCA CGTAGCGCTC CCTGACACGC GGCGTGAAC 720

GAGAAGGCTT GTCGATGAAC TCCAGCTGTT GTGCCAGCCT AGCTTGCGCC TTCTTCTGCT 780

60 GGGTCATGCC CTTCGAGAAA CCCACCTTGG CCACCCTTGT GCTTGAGCGG CGCGCCACCT 840

CAGCAGGCGG CGGCGTGGGG ATGAAGAGGG TGTCTGCTTC CGGAGCAGGC GGGTCGGCGT 900

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	TGA	ACTT	GAA	AGG	CGGT	TGGC	CCCAT	GATGG	ATG	GGGGGG	GAG	CATG	CCAAAG	ACTT	TGGT	TGA	960
	GGAA	AGTGGT	GTTGG	CGTCC	ACCT	TCCAGT	G	CCTGC	AGTTT	GGAAG	CCAGA	CGATT	TGGCGT				1020
5	CGAT	CTCT	TGG	CTCC	GGCT	TGG	AAGG	AGGCTC	GACG	CTCCG	G	TGTG	CCAGAA	CGCA	AAGGGA		1080
	GGAG	CGGC	CAG	CTCT	TGGCT	G	GCAG	ACCCCG	CGCC	CATGTA	CTCT	TGCATT	G	GGCC	AAGGCT		1140
10	GCAG	GGGCAA	GCC	ACCG	GGGA	TGGG	GGGCGC	G	AGGT	TGACTG	CGCA	CCGGAG	GAAG	GCCAA	G		1200
	CTCA	ACCTCG	GTG	AGGT	TTCG	CCCC	CAGACCA	GGG	CGGC	GAGG	CTCG	GGGTCCA	CAA	AGGG	CCA		1260
	AACCG	CCTCG	TCCG	CCCCGA	AACT	GTCCAG	GAC	AGAC	GGC	GGAC	GACGGA	AGG	CCGTG	T			1320
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	CAGC	AGGAAG	GGGG	ACTGGT	CCAT	CGCCCC	TGG	CCAAGCC	ACT	TGGTACGC	CAA	AGATGGC					1440
20	ATCAG	CAGCG	TTTG	CACCAG	GGGG	AGCAGC	CAC	ACCTTGG	AGG	ACAGGGA	GGG	TGCGGAC					1500
	GTCG	ACGGCA	GCAAA	ACGTG	GCT	TGGAGCAA	GTT	TGCCGTCG	CGT	GCCGGCC	TCGG	CGAGCG					1560
	CGAG	CGGCTG	TAGG	AGCGCT	CGGT	TGCCCTC	AGAC	TGGAC	AGT	TGCGCCAG	TGGG	GAGAGCC					1620
25	ATGG	CGACGC	CGGC	CAACAC	TGG	ACGTGCC	ATGG	CGCTGG	TCCT	GACGGC	GCCT	TGGATGG					1680
	CCCG	TCTCG	CGGG	CAGCTC	CAC	TGAGCG	GCAC	CCGAGG	AGCA	CACCCC	GCCA	AAGCTGG					1740
30	GCC	AGGGCGG	CTGC	GGCGAC	GGC	GACGGCC	GCGG	TCGCGG	TCTG	CACCAT	CATC	TTCATC					1800
	TTCG	TATCG	TGGC	GCCTCG	GACA	AAGGATG	CTCG	CTGTCA	CCG	ACGCGAG	GGAC	GTGAGC					1860
	CGG	CTCAGCC	CGCC	CTCCT	CGAC	GTGGCG	AGCC	TGCGG	ATAT	GCTCCT	CGAG	CGGCCA					1920
35	TTGG	GGGTGCG	TTGG	CGCGCG	GCAT	CTCGGG	GTCG	CGGTCA	GCT	ATCGGGG	TGTA	GTCTT					1980
	TGT	TGGTGTCC	AGGT	TGGATGA	GCAG	AGAGAA	ATCC	GGCCCC	TCTA	GGCCCT	CGT	CCCGGGG					2040
40	GCAG	CCCTCC	GGC	AGCGTCT	GGC	GGCCCCCT	GGGG	TCCAGG	GGT	CGATCGA	TGAT	TGGAGAA					2100
	CCCC	CTTTTG	GTGG	GGATGT	CGT	TCCGACT	CCAT	TCCCCAC	A	CCAGGCAA	AGAG	GCAGGC					2160
	CGT	GTTGGAG	AGGG	AGGTGCG	TCT	TGCCGCTC	CAAC	CAGTCG	ACG	TGGCATG	TCT	TCCCGAG					2220
45	CGCA	TCTGCG	CCG	CCTCCT	TGTT	TCCAGGA	CTGC	ACCGGC	ATGT	TCTCGA	CGGC	GATGCG					2280
	GCAG	TAGTAC	CGCC	CAGACAC	GGCG	TGGCC	GTGT	GCCGAT	GGT	GACCAGG	CCG	ACAGGGA					2340
50	GAG	CGCGACG	CCCC	CAGCAGG	AGAC	GACCCC	AGCG	TCGAAA	GCG	ATGTCCC	GGT	GCCTGAA					2400
	GTGG	ACGAGC	CCAG	AGATGG	CCAG	GCGCAT	TGAC	GCGGGG	AAG	GGGAAGG	AGT	TAGGATG					2460
	GGCG	ACGCGG	CCGG	AGTGAA	CCG	CGGCGTG	GTGG	CCGACG	GGG	CTGGAGA	GGC	AGAGGCG					2520
55	GAG	TCATCCG	AGAG	AGGTGT	ATCA	GTGGCT	CTGC	ACAATA	CCC	AGTGTGCG	CCAC	ATCATA					2580
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60	GGAA	AAAAAGAC	GGC	AAAAAAT	TCAC	GAGACAC	ACGA	CTAGTA	GTAC	CCAATA	TACT	CGGCAA					2700
	AAAC	AGTGAC	ACGT	CGTTTTT	GCG	TGTGTCGG	CCGG	TGTGTG	CGAG	TCA	TG	TGTTTT					2760
	TGTC	GTTTTCT	TTCT	TTTTCTC	CAA	ATCGACA	AACC	GTTTGT	CTTT	TGGTTAA	AAA	ACAGAAA					2820
65	CATA	CAAAAT	CAA	ATGAATG	CATT	CA											

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5 GACATCTGAG CAGCTCTCAG CAAAAAAGAC AAATTCGGGG TCTGTAAAAA TGTTTACTGT 3060  
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AGCTAAAATT TTGAGCGGAG CTTACGTGAT AAAATGTCTA TCATGCAAAA AAGGATTGGA 3180  
10 ATTTTTTGAA TTTTTTTTAT TTTTGTGAT TTGTTTCCTG GACGGGTGCA GATAAGCCTG 3240  
GGCACCGAAA CGCCGCACTC AGGCTCATCC TTTTCTATAA AAGAAAAGAA ATACATACAA 3300  
15 TTTCCCTCTG TTTTTTGAGC AAGGGGCACC ACCCACCAA GAGTTTTCAA CTCACATGGT 3360  
ATTAGAGCAT CTACAGCCGG GCGTCTCAA CCAGCTCAT ACGCTTGAGC GGGTCGCCTT 3420  
GGTCACGATT TTTTGACCCA GACGGGCCCC TCAAACGGTC CTAAACGCC CAGGCTGACC 3480  
20 GACAACCCAC ATATCCAGCC CAAATATGGG GTGGATATGG GGGCGCCCGG GCACGCCAGC 3540  
CCGCGGACAC CACACATCTT CAGTTTCTAA TTTGAGATAT CCGGATGTGG AATGCGTTTT 3600  
TGAGGGGTGA CCGGTCCCTG TCCGTGGATG CGCCCGGACG TTTGAGGGGT TGGATTTGCC 3660  
25 AAGTCTGATT AGAGATGCTC TTAGGTGTTT CACCCCCATC CCTTGATGGC TAGGGCAAAC 3720  
TCTCCCCTCC AAACCTTGTC GCGGAGCCTG TGGATTCTTC TCTCCTCTGC CCGCTGCTCC 3780  
30 GCGGCTGAT GCGGGGAGG AGAATCCCGG TGTCTTCGCT TGGTTAGTTG TTTAAGTTAC 3840  
GTACTTTTTT AGTCCTCGCA GGTGCGGCGT TCGGACGTAT GGTCTGCTT CTTTTTTGAG 3900  
35 TTTGTCTTCC GGGCTCTGAT CCTCCTCGAG TTCGTCCATC TGGACGTACT CGACGGAGCT 3960  
CCGGCATAGA TTCCTATCAT CGTCTTGGTG AGGTGAGGTT ATGGTTTCTT GTCATGTGGG 4020  
CAGATTTGGT GCCAGATGCT TCATATCTAT TCAAGGGTTC AGCGGCAACA ACTGCGGCTC 4080  
40 CAGAGCGATG GTCCTTAAGG GCACGTGCAC GAAGACTTCA CGGCTGTTAT CGACAAGGTC 4140  
AAGCCGGCTC CGATAGGGGA GCAGCGACAG CGGCGCGTCA ACCGCTCGTT CTGGCGGCAG 4200  
TAGTGGTTCG TCGGTGCTCT CGGAACCTCG ATGTAATTTT TATGATTTTA GAGATGCTTT 4260  
45 GTACTTCCGA TCGATGAACT CTGATAATAG ATATCTCTTC TCTCGCAAAA AAAGAGAGTT 4320  
TTCAACTGAA AACAAAAGAG TTTCACTAGT TCTTCTTTTA GAAACAGAGT TTTACTAGCA 4380  
50 CTTTTTTTTG CGAGAAGTCG AGTTTCACTA AGTACTAAAC CCACGCAATT ATTCTCAAAA 4440  
AAAAAACCCA CGCAACTGTC TGGATCCATC TTCGTTTTTT CCCCAGAAAT CGTCTGGATC 4500  
55 CATTTTCGTG TGCGAGGCAT CCTCTCATTT TGCACGGCCC AGCTCTCTTC TCGCCGGCGT 4560  
ACGCTGCTAC ATGTCGGCAC TCCACGCAA CAAAAAGAAG CCCAACCGAA AACGCACGCG 4620  
CCTTTCCAGG CTCACCACGG AAAAAAATAC CACGCGCCGC TCACGAGCAA ACCGTGACAA 4680  
60 CAGCCAGCCA GATATGGCAA CGGAGGCACG GGCCGCACAC AGCCACTGAA AACC GCAGCT 4740  
GCTCTTCCGT CCGTCCGTCC CTCCGCCCGT CCGCGCCACT CCACTCGCCT TGCCCCACTC 4800  
65 CCACTCTTCT CTCCCCGCGC ACACCGAGTC GGCACCGGCT CATCACCCAT CACCTCGGCC 4860  
TCGGCCACCG GCAAACCCCC CGATCCGCTT TTGCAGGCAG CGCACTAAAA CCCC GGGGAG 4920

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(2) INFORMATION FOR SEO ID NO: 16:

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(iii) **HYPOTHETICAL: NO**

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- (D) OTHER INFORMATION: /product= "partial cDNA for hexaploid wheat DBE"

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TAT	ATG	CTT	GCA	CCC	AAG	GGA	GAG	TTT	TAT	AAC	TAT	TCT	GGC	TGT	GGG	384
Tyr	Met	Leu	Ala	Pro	Lys	Gly	Glu	Phe	Tyr	Asn	Tyr	Ser	Gly	Cys	Gly	
		115					120					125				



	AAT Asn	ACC Thr	TTC Phe	AAC Asn	TGT Cys	AAT Asn	CAT His	CCT Pro	GTG Val	GTT Val	CGT Arg	CAA Gln	TTC Phe	ATT Ile	GTA Val	GAT Asp	432
		130					135					140					
5	TGT Cys	TTA Leu	AGA Arg	TAC Tyr	TGG Trp	GTG Val	ATG Met	GAA Glu	ATG Met	CAT His	GTT Val	GAT Asp	GGT Gly	TTT Phe	CGT Arg	TTT Phe	480
	145					150					155					160	
10	GAT Asp	CTT Leu	GCA Ala	TCC Ser	ATA Ile	ATG Met	ACC Thr	AGA Arg	GGT Gly	TCC Ser	AGT Ser	CTG Leu	TGG Trp	GAT Asp	CCA Pro	GTT Val	528
					165					170					175		
15	AAC Asn	GTG Val	TAT Tyr	GGA Gly	GCT Ala	CCA Pro	ATA Ile	GAA Glu	GGT Gly	GAC Asp	ATG Met	ATC Ile	ACA Thr	ACA Thr	GGG Gly	ACA Thr	576
				180					185					190			
20	CCT Pro	CTT Leu	GTT Val	ACT Thr	CCA Pro	CCA Pro	CTT Leu	ATT Ile	GAC Asp	ATG Met	ATC Ile	AGC Ser	AAT Asn	GAC Asp	CCA Pro	ATT Ile	624
			195					200					205				
25	CTT Leu	GGA Gly	GGC Gly	GTC Val	AAG Lys	CTC Leu	ATT Ile	GCT Ala	GAA Glu	GCA Ala	TGG Trp	GAT Asp	GCA Ala	GGA Gly	GGC Gly	CTC Leu	672
	210					215						220					
30	TAT Tyr	CAA Gln	GTA Val	GGT Gly	CAA Gln	TTC Phe	CCT Pro	CAC His	TGG Trp	AAT Asn	GTT Val	TGG Trp	TCT Ser	GAG Glu	TGG Trp	AAT Asn	720
	225					230					235					240	
35	GGG Gly	AAG Lys	TAC Tyr	CGG Arg	GAC Asp	ATT Ile	GTG Val	CGC Arg	CAA Gln	TTC Phe	ATT Ile	AAA Lys	GGC Gly	ACT Thr	GAT Asp	GGA Gly	768
					245					250					255		
40	TTT Phe	GCT Ala	GGT Gly	GGT Gly	TTT Phe	GCC Ala	GAA Glu	TGT Cys	CTT Leu	TGT Cys	GGA Gly	AGT Ser	CCA Pro	CAC His	CTA Leu	TAC Tyr	816
			260					265						270			
45	CAG Gln	GCA Ala	GGA Gly	GGA Gly	AGG Arg	AAA Lys	CCT Pro	TGG Trp	CAC His	AGT Ser	ATC Ile	AAC Asn	TTT Phe	GTA Val	TGT Cys	GCA Ala	864
			275					280					285				
50	CAT His	GAT Asp	GGA Gly	TTT Phe	ACA Thr	CTG Leu	GGT Gly	GAT Asp	TTG Leu	GTA Val	ACA Thr	TAT Tyr	AAT Asn	AAC Asn	AAG Lys	TAC Tyr	912
	290					295						300					
55	AAT Asn	TTA Leu	CCA Pro	AAT Asn	GGG Gly	GAG Glu	AAC Asn	AAT Asn	AGA Arg	GAT Asp	GGA Gly	GAA Glu	AAT Asn	CAC His	AAT Asn	CTT Leu	960
	305					310					315					320	
60	AGC Ser	TGG Trp	AAT Asn	TGT Cys	GGG Gly	GAG Glu	GAA Glu	GGA Gly	GAA Glu	TTC Phe	GCA Ala	AGA Arg	TTG Leu	TCT Ser	GTC Val	AAA Lys	1008
					325					330					335		
65	AGA Arg	TTG Leu	AGG Arg	AAG Lys	AGG Arg	CAG Gln	ATG Met	CGC Arg	AAT Asn	TTC Phe	TTT Phe	GTT Val	TGT Cys	CTC Leu	ATG Met	GTT Val	1056
				340				345						350			
70	TCT Ser	CAA Gln	GGA Gly	GTT Val	CCA Pro	ATG Met	TTT Phe	TAC Tyr	ATG Met	GGC Gly	GAT Asp	GAA Glu	TAT Tyr	GGC Gly	CAC His	ACA Thr	1104
			355					360					365				
75	AAA Lys	GGG Gly	GGC Gly	AAC Asn	AAC Asn	AAT Asn	ACA Thr	TAC Tyr	TGC Cys	CAT His	GAT Asp	TCT Ser	TAT Tyr	GTC Val	AAT Asn	TAT Tyr	1152
	370						375					380					

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5	TTT CGC TGG GAT AAA AAA GAA CAA TAC TCT GAC TTG CAC AGA TTC TGC 1200 Phe Arg Trp Asp Lys Lys Glu Gln Tyr Ser Asp Leu His Arg Phe Cys 385 390 395 400
10	TGC CTC ATG ACC AAA TTC CGC AAG GAG TGC GAG GGT CTT GGC CTT GAG 1248 Cys Leu Met Thr Lys Phe Arg Lys Glu Cys Glu Gly Leu Gly Leu Glu 405 410 415
15	GAC TTT CCA ACG GCC GAA CGG CTG CAG TGG CAT GGT CAT CAG CCT GGG 1296 Asp Phe Pro Thr Ala Glu Arg Leu Gln Trp His Gly His Gln Pro Gly 420 425 430
20	AAG CCT GAT TGG TCT GAG AAT AGC CGA TTC GTT GCC TTT TCC ATG AAA 1344 Lys Pro Asp Trp Ser Glu Asn Ser Arg Phe Val Ala Phe Ser Met Lys 435 440 445
25	GAT GAA AGA CAG GGC GAG ATC TAT GTG GCC TTC AAC ACC AGC CAC TTA 1392 Asp Glu Arg Gln Gly Glu Ile Tyr Val Ala Phe Asn Thr Ser His Leu 450 455 460
30	CCG GCC GTT GTT GAG CTC CCA GAG CGC GCA GGG CGC CGG TGG GAA CCG 1440 Pro Ala Val Val Glu Leu Pro Glu Arg Ala Gly Arg Arg Trp Glu Pro 465 470 475 480
35	GTG GTG GAC ACA GGC AAG CCA GCA CCA TAT GAC TTC CTC ACC GAC GAC 1488 Val Val Asp Thr Gly Lys Pro Ala Pro Tyr Asp Phe Leu Thr Asp Asp 485 490 495
40	TTA CCT GAT CGC GCT CTC ACC ATA CAC CAG TTC TCT CAT TTC CTC AAC 1536 Leu Pro Asp Arg Ala Leu Thr Ile His Gln Phe Ser His Phe Leu Asn 500 505 510
45	TCC AAC CTC TAC CCC ATG CTC AGC TAC TCA TCG GTC ATC CTA GTA TTG 1584 Ser Asn Leu Tyr Pro Met Leu Ser Tyr Ser Ser Val Ile Leu Val Leu 515 520 525
50	CGC CCT GAT GTT TGA GAG ACA AAT ATA TAC AGT AAA TAA TAT GTC TAT 1632 Arg Pro Asp Val * Glu Thr Asn Ile Tyr Ser Lys * Tyr Val Tyr 530 535 540
55	ATG TAG TCC TTT GGC GTA TTA TCA GTG TGC ACA ATT GCT CTA TTG CCA 1680 Met * Ser Phe Gly Val Leu Ser Val Cys Thr Ile Ala Leu Leu Pro 545 550 555 560
60	GTG ATC TAT TCG ATA GCG GCC GCG AA 1706 Val Ile Tyr Ser Ile Ala Ala Ala 565
50	(2) INFORMATION FOR SEQ ID NO: 17: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9289 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
55	(ii) MOLECULE TYPE: DNA (genomic)
60	(iii) HYPOTHETICAL: NO (vi) ORIGINAL SOURCE:

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(A) ORGANISM: triticum tauschii

(F) TISSUE TYPE: Endosperm

(ix) FEATURE:

5 (A) NAME/KEY: CDS

(B) LOCATION: 1..9289

(D) OTHER INFORMATION: /product= "genomic sequence of DBE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

10 CGG GAC CGT CCC TTG GCA ACT TGG GTT ACG TTG GGA CCT GAC GCT TCG 48  
 Arg Asp Arg Pro Leu Ala Thr Trp Val Thr Leu Gly Pro Asp Ala Ser  
 570 575 580

15 CTT ATC CGG TGT GCC CTG AGA CGA GAT ATG TGC AGC TCC TAT CGG ATT 96  
 Leu Ile Arg Cys Ala Leu Arg Arg Asp Met Cys Ser Ser Tyr Arg Ile  
 585 590 595 600

20 TGT CGG CAC ATT CGG CGG CTT TGC TGG TCT TGT TTT ACC ATT GTC GAA 144  
 Cys Arg His Ile Arg Arg Leu Cys Trp Ser Cys Phe Thr Ile Val Glu  
 605 610 615

25 ATG TCT TAT AAA CCG GGA TTC CGA GAC TGA TCG GGT CTT CCC GGG AGA 192  
 Met Ser Tyr Lys Pro Gly Phe Arg Asp \* Ser Gly Leu Pro Gly Arg  
 620 625 630

30 AGG TTT ATC CTT CGT TGA CCG TGA GAG CTT ATA ATG GGC TAA GTT GGG 240  
 Arg Phe Ile Leu Arg \* Pro \* Glu Leu Ile Met Gly \* Val Gly  
 635 640 645

35 ACA CCC CTG CAG GGT ATT ATC TTT CGA AAG CCG TGC CCG CGG TTA TGA 288  
 Thr Pro Leu Gln Gly Ile Ile Phe Arg Lys Pro Cys Pro Arg Leu \*  
 650 655 660

40 GGC AGA TGG GAA TTT GTT AAT GTC CGA TTG TAG AGA ACC TGT CAC TTG 336  
 Gly Arg Trp Glu Phe Val Asn Val Arg Leu \* Arg Thr Cys His Leu  
 665 670 675 680

45 ACT TAA TTT AAA ATT CAT CAA CCG TGT GTG TAG CCG TGA TGG TCT CTT 384  
 Thr \* Phe Lys Ile His Gln Pro Cys Val \* Pro \* Trp Ser Leu  
 685 690 695

50 TTC GGC GGA GTC CGG GAA GTG AAC ACG GTT TGA GTT ATG CAT GAA CGT 432  
 Phe Gly Gly Val Arg Glu Val Asn Thr Val \* Val Met His Glu Arg  
 700 705 710

55 AAG TAG TTT CAG GAT CAC TCC TTG ATC ACT TCT AGC TCC GCG ACC GTT 480  
 Lys \* Phe Gln Asp His Ser Leu Ile Thr Ser Ser Ser Ala Thr Val  
 715 720 725

60 GCG TTG TTT CTC TTC TCG CTC TCA TTT GCG TAT GTT AGC CAC CAT ATA 528  
 Ala Leu Phe Leu Phe Ser Leu Ser Phe Ala Tyr Val Ser His His Ile  
 730 735 740

55 TGC TTA GTG TCT GCT GCA GCT CCA CCT CAT TAC CCC TTC CTT TCC TAT 576  
 Cys Leu Val Ser Ala Ala Ala Pro Pro His Tyr Pro Phe Leu Ser Tyr  
 745 750 755 760

60 AAG CTT AAA TAG TCT TGA TCT CGC GGG TGT GAG ATT GCT GAG TCC TCG 624  
 Lys Leu Lys \* Ser \* Ser Arg Gly Cys Glu Ile Ala Glu Ser Ser  
 765 770 775

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	TGA	CTT	ACA	GAT	TCT	ACC	AAA	ACA	GTT	GCA	GGT	GTC	GAC	GAT	GCC	AGT	672
	*	Leu	Thr	Asp	Ser	Thr	Lys	Thr	Val	Ala	Gly	Val	Asp	Asp	Ala	Ser	
				780					785						790		
5	GCA	GGT	GAC	GCA	ACC	GAG	CTC	AAG	TGG	GAG	TTC	GAC	GAG	GAA	CGT	GGT	720
	Ala	Gly	Asp	Ala	Thr	Glu	Leu	Lys	Trp	Glu	Phe	Asp	Glu	Glu	Arg	Gly	
			795					800					805				
10	CGT	TAC	TAT	GTT	TCT	TTT	CCT	GAT	GAT	CAG	TAG	TGG	AGC	CCA	GTT	GGG	768
	Arg	Tyr	Tyr	Val	Ser	Phe	Pro	Asp	Asp	Gln	*	Trp	Ser	Pro	Val	Gly	
		810					815					820					
15	ACG	ATC	GGG	GAT	CTA	GCA	TTT	GGG	GTT	ATC	TTA	ATT	TCT	TTT	AGA	TTT	816
	Thr	Ile	Gly	Asp	Leu	Ala	Phe	Gly	Val	Ile	Leu	Ile	Ser	Phe	Arg	Phe	
	825					830					835					840	
20	GAC	CGT	AAT	CGG	TCT	ATG	TGT	GGA	TTT	TGG	ATG	ATG	TAT	GAA	TTA	TTT	864
	Asp	Arg	Asn	Arg	Ser	Met	Cys	Gly	Phe	Trp	Met	Met	Tyr	Glu	Leu	Phe	
					845					850					855		
	ATG	TAT	TGT	GTG	AAG	TGG	CGA	TTG	TAA	GCC	AAC	TCT	CGT	TAT	CCC	ATT	912
	Met	Tyr	Cys	Val	Lys	Trp	Arg	Leu	*	Ala	Asn	Ser	Arg	Tyr	Pro	Ile	
				860					865					870			
25	CTT	GTT	CAT	TAC	ATG	GGA	TTG	TGT	GAA	GAT	GAC	CCT	TCT	TGC	GAC	AAA	960
	Leu	Val	His	Tyr	Met	Gly	Leu	Cys	Glu	Asp	Asp	Pro	Ser	Cys	Asp	Lys	
			875					880					885				
30	ACC	ACA	ATG	CGG	TTA	TGC	CTC	TAA	GTC	GTG	CCT	CGA	CAC	GTG	GGA	GAT	1008
	Thr	Thr	Met	Arg	Leu	Cys	Leu	*	Val	Val	Pro	Arg	His	Val	Gly	Asp	
			890				895					900					
35	ATA	GCC	GCA	TCG	TGG	GCG	TTA	CAC	GCA	AGT	CTT	CAT	AGC	AAC	CAA	AAC	1056
	Ile	Ala	Ala	Ser	Trp	Ala	Leu	His	Ala	Ser	Leu	His	Ser	Asn	Gln	Asn	
	905					910					915					920	
40	TCC	TCT	CCG	CAT	TAC	AAG	CCA	CCA	ATC	GCA	GCC	ACC	ATG	ACT	TTC	TTC	1104
	Ser	Ser	Pro	His	Tyr	Lys	Pro	Pro	Ile	Ala	Ala	Thr	Met	Thr	Phe	Phe	
					925					930					935		
	ACC	ACT	GTC	AAT	GCC	ATG	AAA	ATC	TAT	ATG	TAG	ACA	TGT	CCC	ATT	GCA	1152
	Thr	Thr	Val	Asn	Ala	Met	Lys	Ile	Tyr	Met	*	Thr	Cys	Pro	Ile	Ala	
				940					945					950			
45	TCG	GCA	AGA	AAG	CGA	AGC	TTC	ACG	GCA	CAC	CTT	CAT	GAA	GCC	TCT	CTG	1200
	Ser	Ala	Arg	Lys	Arg	Ser	Phe	Thr	Ala	His	Leu	His	Glu	Ala	Ser	Leu	
			955					960					965				
50	GCC	GAA	GAC	AAG	GAT	GCG	CCC	GAC	CGG	ATC	AAT	TCC	TAT	CTA	GAT	ACC	1248
	Ala	Glu	Asp	Lys	Asp	Ala	Pro	Asp	Arg	Ile	Asn	Ser	Tyr	Leu	Asp	Thr	
		970					975					980					
55	TAG	TGG	AGC	CAT	GCG	CCA	ATA	GCG	GAG	ATC	TCC	GAG	AGG	AAG	ACC	GGA	1296
	*	Trp	Ser	His	Ala	Pro	Ile	Ala	Glu	Ile	Ser	Glu	Arg	Lys	Thr	Gly	
	985					990					995					1000	
60	ACT	CGT	CGG	ACG	TCG	GCG	TCC	AAA	TCG	AGG	AGG	CCG	GCA	TGA	AGC	ACA	1344
	Thr	Arg	Arg	Thr	Ser	Ala	Ser	Lys	Ser	Arg	Arg	Pro	Ala	*	Ser	Thr	
					1005					1010					1015		
	TCG	AGG	ATG	GTG	ATC	CCC	ATA	CGG	GTA	GAT	CGG	GTC	GGC	CGC	CAT	CTC	1392
	Ser	Arg	Met	Val	Ile	Pro	Ile	Arg	Val	Asp	Arg	Val	Gly	Arg	His	Leu	
				1020					1025					1030			

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**Figure 1**

	ACA	CCG	AGA	TTA	GGA	TGC	TTA	AAA	CGG	TTT	TTT	TGG	CAC	TAG	CAT	TAT	1440
	Thr	Pro	Arg	Leu	Gly	Cys	Leu	Lys	Arg	Phe	Phe	Trp	His	*	His	Tyr	
			1035					1040					1045				
5	TTT	GCA	TCA	TCC	GTT	GGA	GAG	AAC	ATG	AGA	GAG	CCC	CAT	TTC	TTC	CAC	1488
	Phe	Ala	Ser	Ser	Val	Gly	Glu	Asn	Met	Arg	Glu	Pro	His	Phe	Phe	His	
		1050					1055					1060					
10	GGT	TCT	ACC	TAT	GGG	ATC	TTG	TTC	TGC	TTG	CAA	CCG	GGC	CTC	ACG	GAA	1536
	Gly	Ser	Thr	Tyr	Gly	Ile	Leu	Phe	Cys	Leu	Gln	Pro	Gly	Leu	Thr	Glu	
	1065					1070					1075					1080	
	AAC	CCG	CGC	CAG	CGG	ACC	CAC	CCC	ATG	CTA	GCA	GGG	CAC	GGC	ACC	CGC	1584
15	Asn	Pro	Arg	Gln	Arg	Thr	His	Pro	Met	Leu	Ala	Gly	His	Gly	Thr	Arg	
				1085					1090						1095		
	AGC	GGC	CGG	TCC	AAA	TGG	ACG	GTG	AGA	ACC	GCA	ACG	CGA	CAC	GCC	CGG	1632
20	Ser	Gly	Arg	Ser	Lys	Trp	Thr	Val	Arg	Thr	Ala	Thr	Arg	His	Ala	Arg	
				1100					1105					1110			
	CAC	TGT	CAG	CAA	AGC	GAG	AGC	GCG	CGC	ACG	GCA	CAC	GCA	CGC	TCG	GAC	1680
	His	Cys	Gln	Gln	Ser	Glu	Ser	Ala	Arg	Thr	Ala	His	Ala	Arg	Ser	Asp	
			1115					1120					1125				
25	GAA	CGG	ACG	GTG	CGA	TCG	ATC	CCT	CCC	CCC	TCG	CTC	AAC	CAC	AGT	AGT	1728
	Glu	Arg	Thr	Val	Arg	Ser	Ile	Pro	Pro	Pro	Ser	Leu	Asn	His	Ser	Ser	
		1130					1135					1140					
30	ACC	CTG	CCA	CAC	TAT	CAC	GCA	CGC	ACT	CGA	GTC	ACA	CCT	CCC	ACG	AAG	1776
	Thr	Leu	Pro	His	Tyr	His	Ala	Arg	Thr	Arg	Val	Thr	Pro	Pro	Thr	Lys	
	1145					1150					1155					1160	
	AAC	CAA	CAG	GAG	GCG	CGG	ATC	CCA	CCG	ATA	AAT	AAC	CCC	GCC	TCG	CCG	1824
35	Asn	Gln	Gln	Glu	Ala	Arg	Ile	Pro	Pro	Ile	Asn	Asn	Pro	Ala	Ser	Pro	
				1165						1170					1175		
	CTC	CTC	CCC	AAA	ATC	AAT	CAC	CGA	TCG	CTC	GGG	GTT	CCC	GGC	ATG	ACG	1872
40	Leu	Leu	Pro	Lys	Ile	Asn	His	Arg	Ser	Leu	Gly	Val	Pro	Gly	Met	Thr	
				1180					1185					1190			
	ATG	ATG	GCC	ATG	GCC	AAG	GCG	CCC	TGC	CTC	TGC	GCG	CGC	CCG	TCC	CTC	1920
	Met	Met	Ala	Met	Ala	Lys	Ala	Pro	Cys	Leu	Cys	Ala	Arg	Pro	Ser	Leu	
			1195					1200					1205				
45	GCC	GCG	CGC	GCG	AGG	CGG	CCG	GGG	CCG	GGG	CCG	GCG	CCG	CGC	CTG	CGA	1968
	Ala	Ala	Arg	Ala	Arg	Arg	Pro	Gly	Pro	Gly	Pro	Ala	Pro	Arg	Leu	Arg	
		1210					1215					1220					
50	CGG	TGG	CGA	CCC	AAT	GCG	ACG	GCG	GGG	AAG	GGG	GTC	GGC	GAG	GTG	TGC	2016
	Arg	Trp	Arg	Pro	Asn	Ala	Thr	Ala	Gly	Lys	Gly	Val	Gly	Glu	Val	Cys	
	1225					1230					1235					1240	
	GCC	GCG	GTT	GTC	GAG	GCG	GCG	ACG	AAG	GCC	GAG	GAT	GAG	GAC	GAC	GAC	2064
55	Ala	Ala	Val	Val	Glu	Ala	Ala	Thr	Lys	Ala	Glu	Asp	Glu	Asp	Asp	Asp	
				1245					1250					1255			
	GAG	GAG	GAG	GCG	GTG	GCG	GAG	GAC	AGG	TAC	GCG	CTC	GGC	GGC	GCG	TGC	2112
60	Glu	Glu	Glu	Ala	Val	Ala	Glu	Asp	Arg	Tyr	Ala	Leu	Gly	Gly	Ala	Cys	
				1260					1265					1270			
	AGG	GTG	CTC	GCC	GGA	ATG	CCC	GCG	CCG	CTG	GGC	GCC	ACC	GCG	CTC	GCC	2160
	Arg	Val	Leu	Ala	Gly	Met	Pro	Ala	Pro	Leu	Gly	Ala	Thr	Ala	Leu	Ala	
		1275						1280					1285				

	GGC GGG GTC AAT TTC GCC GTC TAC TCC GGT GGA GCC ACC GCC GCG GCG	2208
	Gly Gly Val Asn Phe Ala Val Tyr Ser Gly Gly Ala Thr Ala Ala Ala	
	1290 1295 1300	
5	CTC TGC CTC TTC ACG CCA GAA GAT CTC AAG GCG GTG GGG TTG CCT CCC	2256
	Leu Cys Leu Phe Thr Pro Glu Asp Leu Lys Ala Val Gly Leu Pro Pro	
	1305 1310 1315 1320	
10	GAG TAG AGT TCA TCA GCT TTG CGT GCG CCG CGC GCC CCC TTT TCT GGC	2304
	Glu * Ser Ser Ser Ala Leu Arg Ala Pro Arg Ala Pro Phe Ser Gly	
	1325 1330 1335	
15	CTG CGA TTT AAG TTT TGT ACT GGG GGA AAT GCT GCA GGA TAG GGT GAC	2352
	Leu Arg Phe Lys Phe Cys Thr Gly Gly Asn Ala Ala Gly * Gly Asp	
	1340 1345 1350	
20	GGA GGA GGT TTC CCT TGA CCC CCT GAT GAA TCG GAC TGG GAA CGT GTG	2400
	Gly Gly Gly Phe Pro * Pro Pro Asp Glu Ser Asp Trp Glu Arg Val	
	1355 1360 1365	
25	GCA TGT CTT CAT TGA AGG CGA GCT GCA CGA CAT GCT TTA CGG GTA CAG	2448
	Ala Cys Leu His * Arg Arg Ala Ala Arg His Ala Leu Arg Val Gln	
	1370 1375 1380	
30	GTT CGA CGG CAC CTT TGC TCC TCA CTG CGG GCA CTA CCT TGA TAT TTC	2496
	Val Arg Arg His Leu Cys Ser Ser Leu Arg Ala Leu Pro * Tyr Phe	
	1385 1390 1395 1400	
35	CAA TGT CGT GGT GGA TCC TTA TGC TAA GGT GAT CAT ACT TTA GCT TTA	2544
	Gln Cys Arg Gly Gly Ser Leu Cys * Gly Asp His Thr Leu Ala Leu	
	1405 1410 1415	
40	CCT GCA TCT TGG TAT TTA CAG TAG AAA TTG TTA CGT GGA CCC TTA TTT	2592
	Pro Ala Ser Trp Tyr Leu Gln * Lys Leu Leu Arg Gly Pro Leu Phe	
	1420 1425 1430	
45	GTT GCC TTT TGT GTT GCT CTA GGC AGT GAT AAG CCG AGG GGA GTA TGG	2640
	Val Ala Phe Cys Val Ala Leu Gly Ser Asp Lys Pro Arg Gly Val Trp	
	1435 1440 1445	
50	CGT TCC GGC GCG TGG TAA CAA TTG CTG GCC TCA GAT GGC TGG CAT GAT	2688
	Arg Ser Gly Ala Trp * Gln Leu Leu Ala Ser Asp Gly Trp His Asp	
	1450 1455 1460	
55	CCC TCT TCC ATA TAG CAC GGT ATG CCT GAT TGC TGA AAA TAT TGG CTG	2736
	Pro Ser Ser Ile * His Gly Met Pro Asp Cys * Lys Tyr Trp Leu	
	1465 1470 1475 1480	
60	CAT TTG TTT CTC TCT TTT TCT CAT ATT TTT CTC CTG TCT TTC ACT TGT	2784
	His Leu Phe Leu Ser Phe Ser His Ile Phe Leu Leu Ser Phe Thr Cys	
	1485 1490 1495	
65	ACT ACA TTG CCT CAG ACA GTC ATG ATC AAA GAG AGC AGT GTC ATT AGA	2832
	Thr Thr Leu Pro Gln Thr Val Met Ile Lys Glu Ser Ser Val Ile Arg	
	1500 1505 1510	
70	CAT TTG TAG TTG TCT GCT GAC TTT GAC CAA AAC TTG TAA TTT ACT GTT	2880
	His Leu * Leu Ser Ala Asp Phe Asp Gln Asn Leu * Phe Thr Val	
	1515 1520 1525	
75	GTT AAA GGT CCT TGA ATC ATA TTT TTT TAT AAT ATT ATG TTT GCA AGT	2928
	Val Lys Gly Pro * Ile Ile Phe Phe Tyr Asn Ile Met Phe Ala Ser	
	1530 1535 1540	

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	GGA	AGT	AAA	GTG	AAA	TTG	CAT	CTA	GTA	TTT	GTT	GTT	GCT	GTC	TTA	GTC	2976
	Gly	Ser	Lys	Val	Lys	Leu	His	Leu	Val	Phe	Val	Val	Ala	Val	Leu	Val	
	1545					1550					1555					1560	
5	GTT	TAA	TTG	GAC	ATG	CAG	TAA	AAA	GGT	TTG	CAT	CTG	CAG	TTT	GAT	TGG	3024
	Val	*	Leu	Asp	Met	Gln	*	Lys	Gly	Leu	His	Leu	Gln	Phe	Asp	Trp	
					1565					1570					1575		
10	GAA	GGC	GAC	CTA	CCT	CTA	AGA	TAT	CCT	CAA	AAG	GAC	CTG	GTA	ATA	TAT	3072
	Glu	Gly	Asp	Leu	Pro	Leu	Arg	Tyr	Pro	Gln	Lys	Asp	Leu	Val	Ile	Tyr	
				1580					1585					1590			
15	GAG	ATG	CAC	TTG	CGT	GGA	TTC	ACG	AAG	CAT	GAT	TCA	AGC	AAT	GTA	GAA	3120
	Glu	Met	His	Leu	Arg	Gly	Phe	Thr	Lys	His	Asp	Ser	Ser	Asn	Val	Glu	
			1595					1600					1605				
20	CAT	CCG	GGT	ACT	TTC	ATT	GGA	GCT	GTG	TCG	AAG	CTT	GAC	TAT	TTG	AAG	3168
	His	Pro	Gly	Thr	Phe	Ile	Gly	Ala	Val	Ser	Lys	Leu	Asp	Tyr	Leu	Lys	
		1610					1615					1620					
25	GTA	CAG	CTG	TAC	TTG	CTG	ACT	ACA	TAG	GAT	AAT	TTT	TAA	AGA	AAG	CTA	3216
	Val	Gln	Leu	Tyr	Leu	Leu	Thr	Thr	*	Asp	Asn	Phe	*	Arg	Lys	Leu	
		1625				1630					1635					1640	
30	CAT	ATT	AGC	CAG	AAT	TTG	GGT	TAT	TAC	AAA	AAC	TAC	TGC	ATA	CTA	TAG	3264
	His	Ile	Ser	Gln	Asn	Leu	Gly	Tyr	Tyr	Lys	Asn	Tyr	Cys	Ile	Leu	*	
					1645					1650					1655		
35	CAG	TTA	CAT	GCT	CAT	TAT	CGA	GGA	GAT	GCT	CAC	ACG	CAT	CTT	ATT	TGG	3312
	Gln	Leu	His	Ala	His	Tyr	Arg	Gly	Asp	Ala	His	Thr	His	Leu	Ile	Trp	
				1660					1665					1670			
40	ATT	TAA	TAC	CCA	ATT	CTG	TTT	TGA	TAT	TGG	ACT	GTT	CCC	TCT	ACA	GGA	3360
	Ile	*	Tyr	Pro	Ile	Leu	Phe	*	Tyr	Trp	Thr	Val	Pro	Ser	Thr	Gly	
			1675					1680					1685				
45	GCT	TGG	AGT	TAA	TTG	TAT	TGA	ATT	AAT	GCC	CTG	CCA	TGA	GTT	CAA	CGA	3408
	Ala	Trp	Ser	*	Leu	Tyr	*	Ile	Asn	Ala	Leu	Pro	*	Val	Gln	Arg	
		1690						1695				1700					
50	GCT	GGA	GTA	CTC	AAC	CTC	TTC	TTC	CAA	GTA	AGG	ACA	TGA	ATT	TAG	TAT	3456
	Ala	Gly	Val	Leu	Asn	Leu	Phe	Phe	Gln	Val	Arg	Thr	*	Ile	*	Tyr	
		1705				1710					1715					1720	
55	TAG	CCT	GCC	AGC	ACT	GTT	TGA	GTG	AGA	GTT	CAT	ACA	CAT	TTT	GTG	CCT	3504
	*	Pro	Ala	Ser	Thr	Val	*	Val	Arg	Val	His	Thr	His	Phe	Val	Pro	
					1725					1730					1735		
60	GCA	TAA	CTG	ATA	TTT	GTT	CAA	ACT	ATT	TTT	TTT	AGC	AGT	CAC	TCA	ACA	3552
	Ala	*	Leu	Ile	Phe	Val	Gln	Thr	Ile	Phe	Phe	Ser	Ser	His	Ser	Thr	
				1740					1745					1750			
65	GTT	TTA	CAT	ATA	TAT	ATA	ATA	TAG	ACT	ATT	CGT	CAC	CCT	GGG	TGA	GGA	3600
	Val	Leu	His	Ile	Tyr	Ile	Ile	*	Thr	Ile	Arg	His	Pro	Gly	*	Gly	
			1755					1760					1765				
70	ATA	GTT	ATT	CTT	CAC	CCA	CCT	CTA	TTT	TAA	CAT	CTA	TGC	ACC	GTA	ATT	3648
	Ile	Val	Ile	Leu	His	Pro	Pro	Leu	Phe	*	His	Leu	Cys	Thr	Val	Ile	
		1770					1775					1780					
75	TTA	CGT	TTC	GTA	AAT	TTG	TCT	TAT	TTT	AGA	GAT	AAA	AAG	AGA	ACG	TAA	3696
	Leu	Arg	Phe	Val	Asn	Leu	Ser	Tyr	Phe	Arg	Asp	Lys	Lys	Arg	Thr	*	
		1785				1790					1795					1800	

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	GAA	AAC	CTA	TAA	TCG	TCG	TAA	AAA	AAA	ATA	TGT	TAC	GTA	AAA	TTA	CAA	3744
	Glu	Asn	Leu	*	Ser	Ser	*	Lys	Lys	Ile	Cys	Tyr	Val	Lys	Leu	Gln	
					1805					1810						1815	
5	ATG	TAA	AAA	CAT	AGT	GTA	AAA	TGT	ACA	TAA	AAT	ACA	TTT	TTT	GAC	CTA	3792
	Met	*	Lys	His	Ser	Val	Lys	Cys	Thr	*	Asn	Thr	Phe	Phe	Asp	Leu	
					1820				1825							1830	
10	TAT	TTT	TTT	TGT	TAA	TGC	CAA	ATT	TTA	TAC	AGT	AAA	TCA	ATA	TGA	ATG	3840
	Tyr	Phe	Phe	Cys	*	Cys	Gln	Ile	Leu	Tyr	Ser	Lys	Ser	Ile	*	Met	
					1835				1840							1845	
15	TAA	CTA	TTT	GTA	TTT	CAA	ATG	TAA	TTT	ATT	TAT	GAA	ATG	GTC	GTA	AGA	3888
	*	Leu	Phe	Val	Phe	Gln	Met	*	Phe	Ile	Tyr	Glu	Met	Val	Val	Arg	
					1850				1855							1860	
20	TTA	CCT	CGG	GTG	AAG	AAT	AAC	TTA	TTC	TGC	ACC	CTG	GGT	GAT	GAA	TAG	3936
	Leu	Pro	Arg	Val	Lys	Asn	Asn	Leu	Phe	Cys	Thr	Leu	Gly	Asp	Glu	*	
					1865				1870							1880	
25	TAA	CAC	TAT	ATA	TAT	ATA	TAT	ATA	TAT	ATA	TAT	ATA	TAT	ATA	CCG	GCT	3984
	*	His	Tyr	Ile	Tyr	Ile	Tyr	Ile	Tyr	Ile	Tyr	Ile	Tyr	Ile	Pro	Ala	
					1885					1890						1895	
30	GCT	GCT	AAT	GAT	GTT	AAT	ATT	TCG	CAA	GTA	CCT	AAG	CTG	GAT	TTT	TCT	4032
	Ala	Ala	Asn	Asp	Val	Asn	Ile	Ser	Gln	Val	Pro	Lys	Leu	Asp	Phe	Ser	
					1900					1905						1910	
35	CCA	TGA	GAC	ATC	AAT	CCA	TAA	TTG	AAA	TTG	GTC	ACG	ACA	GTT	GAA	TAG	4080
	Pro	*	Asp	Ile	Asn	Pro	*	Leu	Lys	Leu	Val	Thr	Thr	Val	Glu	*	
					1915					1920						1925	
40	TTG	ATA	GCT	GAA	AAT	GAA	ATC	CAG	CAT	GCT	ACT	GTC	TTG	CCA	TCT	CCA	4128
	Leu	Ile	Ala	Glu	Asn	Glu	Ile	Gln	His	Ala	Thr	Val	Leu	Pro	Ser	Pro	
					1930				1935							1940	
45	GAC	TTG	CTA	ACA	TGA	ATT	TTG	TCT	GCC	TAC	CTG	TCA	TTT	GTA	CCA	ACG	4176
	Asp	Leu	Leu	Thr	*	Ile	Leu	Ser	Ala	Tyr	Leu	Ser	Phe	Val	Pro	Thr	
					1945					1950						1960	
50	TTC	CCA	ATT	GCC	CTC	TCA	TTA	TTC	GTG	TGT	ACC	ATG	CAT	ATG	TGT	TTT	4224
	Phe	Pro	Ile	Ala	Leu	Ser	Leu	Phe	Val	Cys	Thr	Met	His	Met	Cys	Phe	
					1965					1970						1975	
55	AAC	ATG	ATT	ATT	GTT	GGC	TAT	ATT	TCT	CTT	TGG	AAA	CAT	GAC	TAA	TTT	4272
	Asn	Met	Ile	Ile	Val	Gly	Tyr	Ile	Ser	Leu	Trp	Lys	His	Asp	*	Phe	
					1980					1985						1990	
60	ATC	ACC	CGT	TTT	GTA	TAA	ACT	GCT	TGT	TTT	CAT	ATC	AGG	ATG	AAC	TTT	4320
	Ile	Thr	Arg	Phe	Val	*	Thr	Ala	Cys	Phe	His	Ile	Arg	Met	Asn	Phe	
					1995					2000						2005	
55	TGG	GGA	TAT	TCT	ACC	ATA	AAC	TTC	TTT	TCA	CCA	ATG	ACG	AGA	TAC	ACA	4368
	Trp	Gly	Tyr	Ser	Thr	Ile	Asn	Phe	Phe	Ser	Pro	Met	Thr	Arg	Tyr	Thr	
					2010					2015						2020	
60	TCA	GGC	GGG	ATA	AAA	AAC	TGT	GGG	CGT	GAT	GCC	ATA	AAT	GAG	TTC	AAA	4416
	Ser	Gly	Gly	Ile	Lys	Asn	Cys	Gly	Arg	Asp	Ala	Ile	Asn	Glu	Phe	Lys	
					2025				2030							2040	
60	ACT	TTT	GTA	AGA	GAG	GCT	CAC	AAA	CGG	GGA	ATT	GAG	GTA	AGC	AAG	TCG	4464
	Thr	Phe	Val	Arg	Glu	Ala	His	Lys	Arg	Gly	Ile	Glu	Val	Ser	Lys	Ser	
					2045					2050						2055	



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	TAC GAG TTA GTT GCT CCT TTT GAA CTT ATC AAT TTG ATG CGA AGA CAT	4512
	Tyr Glu Leu Val Ala Pro Phe Glu Leu Ile Asn Leu Met Arg Arg His	
	2060 2065 2070	
5	GTT ACT GCT AGG TGA TCC TGG ATG TTG TCT TCA ACC ATA CAG CTG AGG	4560
	Val Thr Ala Arg * Ser Trp Met Leu Ser Ser Thr Ile Gln Leu Arg	
	2075 2080 2085	
10	GTA ATG AGA ATG GTC CAA TAT TAT CAT TTA GGG GGG TCG ATA ATA CTA	4608
	Val Met Arg Met Val Gln Tyr Tyr His Leu Gly Gly Ser Ile Ile Leu	
	2090 2095 2100	
15	CAT ACT ATA TGC TTG CAC CCA AGG TGA CAG ATC TTT CTT GCT GCG TAA	4656
	His Thr Ile Cys Leu His Pro Arg * Gln Ile Phe Leu Ala Ala *	
	2105 2110 2115 2120	
20	TTG TTC TTT CAT AGA TGT ATA GAG CAT AGA TGT GTT ATG TAG TAG TTC	4704
	Leu Phe Phe His Arg Cys Ile Glu His Arg Cys Val Met * * Phe	
	2125 2130 2135	
25	TTT TTC AAG GGG ATT ATG TTC ATG CAG GGA GAG TTT TAT AAC TAT TCT	4752
	Phe Phe Lys Gly Ile Met Phe Met Gln Gly Glu Phe Tyr Asn Tyr Ser	
	2140 2145 2150	
30	GGC TGT GGG AAT ACC TTC AAC TGT AAT CAT CCT GTG GTT CGT CAA TTC	4800
	Gly Cys Gly Asn Thr Phe Asn Cys Asn His Pro Val Val Arg Gln Phe	
	2155 2160 2165	
35	ATT GTA GAT TGT TTA AGG TAC AGA TAT ACA TTT TAC TTC TAG AAC TAC	4848
	Ile Val Asp Cys Leu Arg Tyr Arg Tyr Thr Phe Tyr Phe * Asn Tyr	
	2170 2175 2180	
40	TTT TTC ATT TCT TTT GCT GCT TGT CAT TTT GAT ATG ATT AAT TTG CAA	4896
	Phe Phe Ile Ser Phe Ala Ala Cys His Phe Asp Met Ile Asn Leu Gln	
	2185 2190 2195 2200	
45	GCT TGT GGG GGT AAA TCT TTT GGT CAG CAT ATT GTA TCT TTA AAT GTC	4944
	Ala Cys Gly Gly Lys Ser Phe Gly Gln His Ile Val Ser Leu Asn Val	
	2205 2210 2215	
50	ACA AAT ACT AAT GTC CTG GTG CTT ATT GAT TTG GCA TCT TCA AAT TCT	4992
	Thr Asn Thr Asn Val Leu Val Leu Ile Asp Leu Ala Ser Ser Asn Ser	
	2220 2225 2230	
55	TCT CCA ATG AAA AGG GAA AAA TCT ACT GTA TGT CTC GTC AAC TAA TTT	5040
	Ser Pro Met Lys Arg Glu Lys Ser Thr Val Cys Leu Val Asn * Phe	
	2235 2240 2245	
60	ACT TTT GTT TTG CAG ATA CTG GGT GAT GGA AAT GCA TGT TGA TGG TTT	5088
	Thr Phe Val Leu Gln Ile Leu Gly Asp Gly Asn Ala Cys * Trp Phe	
	2250 2255 2260	
65	TCG TTT TGA TCT TGC ATC CAT AAT GAC CAG AGG TTC CAG GTA ATT TGT	5136
	Ser Phe * Ser Cys Ile His Asn Asp Gln Arg Phe Gln Val Ile Cys	
	2265 2270 2275 2280	
70	ATT TAT TGT TTG TTT GCG TGT TGC CTT TTC AGA AGA TTC TTA AAA GAA	5184
	Ile Tyr Cys Leu Phe Ala Cys Cys Leu Phe Arg Arg Phe Leu Lys Glu	
	2285 2290 2295	
75	TGT TTC TTT TAC AAG TCT GTG GGA TCC AGT TAA CGT GTA TGG AGC TCC	5232
	Cys Phe Phe Tyr Lys Ser Val Gly Ser Ser * Arg Val Trp Ser Ser	
	2300 2305 2310	

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	AAT AGA AGG TGA CAT GAT CAC AAC AGG GAC ACC TCT TGT TAC TCC ACC	5280
	Asn Arg Arg * His Asp His Asn Arg Asp Thr Ser Cys Tyr Ser Thr	
	2315 2320 2325	
5	ACT TAT TGA CAT GAT CAG CAA TGA CCC AAT TCT TGG AGG CGT CAA GGT	5328
	Thr Tyr * His Asp Gln Gln * Pro Asn Ser Trp Arg Arg Gln Gly	
	2330 2335 2340	
10	ACT TGT TTC ATC CAA CAC CTG TTG TCT GTG TGC ATT CAA TTG TTT TAA	5376
	Thr Cys Phe Ile Gln His Leu Leu Ser Val Cys Ile Gln Leu Phe *	
	2345 2350 2355 2360	
15	TAT GGT AAT GAT CAA TTT CCC AAT GTT GAT AAG GAA AAA AAA TGC AAG	5424
	Tyr Gly Asn Asp Gln Phe Pro Asn Val Asp Lys Glu Lys Lys Cys Lys	
	2365 2370 2375	
20	TAG CTC TCT TTA TCT GCT TCT TGT GAG TTA TGC TAA ACA TGT AGA TAC	5472
	* Leu Ser Leu Ser Ala Ser Cys Glu Leu Cys * Thr Cys Arg Tyr	
	2380 2385 2390	
25	TAC TAT ATT TCA ACT GTA TAT ACT TGA CAT ATT ATT GCT TCC TTG GGA	5520
	Tyr Tyr Ile Ser Thr Val Tyr Thr * His Ile Ile Ala Ser Leu Gly	
	2395 2400 2405	
30	GGC TCT CTT ATT CCT TTC CCC CGT TGC AAT TAT AGC TCA TTG CTG AAG	5568
	Gly Ser Leu Ile Pro Phe Pro Arg Cys Asn Tyr Ser Ser Leu Leu Lys	
	2410 2415 2420	
35	CAT GGG ATG CAG GAG GCC TCT ATC AAG TAG GTC AAT TCC CTC ACT GGA	5616
	His Gly Met Gln Glu Ala Ser Ile Lys * Val Asn Ser Leu Thr Gly	
	2425 2430 2435 2440	
40	ATG TTT GGT CTG AGT GGA ATG GGA AGG TAA GGT ACC TGT TAA AAG TTT	5664
	Met Phe Gly Leu Ser Gly Met Gly Arg * Gly Thr Cys * Lys Phe	
	2445 2450 2455	
45	GAA TGG CAA ATA CTG ATA GAA ATA TAA CTT ATA TTT GCG ACA TAT ATA	5712
	Glu Trp Gln Ile Leu Ile Glu Ile * Leu Ile Phe Ala Thr Tyr Ile	
	2460 2465 2470	
50	GAT AAA GCA AAA TAA TAC GCA TTC CAC CTG AAC TTT AAA GGG GCA CGC	5760
	Asp Lys Ala Lys * Tyr Ala Phe His Leu Asn Phe Lys Gly Ala Arg	
	2475 2480 2485	
55	AGA ATT ATC CCG CAT CTG TCT ACA AGA ATG ATA ACA CAT GTG CTG AAT	5808
	Arg Ile Ile Pro His Leu Ser Thr Arg Met Ile Thr His Val Leu Asn	
	2490 2495 2500	
60	AGT GAA GTA CTA CTT CTC AAA TGT CTG AAT GAA CGC ACT AAC TCT TGT	5856
	Ser Glu Val Leu Leu Leu Lys Cys Leu Asn Glu Arg Thr Asn Ser Cys	
	2505 2510 2515 2520	
65	GAG TGT CAA CCG AGC AAG AAA TAT TTG AGT TTT CTG CAA GAA ATT GTT	5904
	Glu Cys Gln Pro Ser Lys Lys Tyr Leu Ser Phe Leu Gln Glu Ile Val	
	2525 2530 2535	
70	CAT GTT GTG CTG TAT TAT ACT CCC TCC GTC CGA AAT TAT TTG TCG GAG	5952
	His Val Val Leu Tyr Tyr Thr Pro Ser Val Arg Asn Tyr Leu Ser Glu	
	2540 2545 2550	
75	AAA TGG ATG TAT CTA GAC GTA TTT TAG TTC TAG ATA CAT CCA TTT TTA	6000
	Lys Trp Met Tyr Leu Asp Val Phe * Phe * Ile His Pro Phe Leu	
	2555 2560 2565	

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	TCC	ATT	TCT	GCA	ACA	AGT	AGT	TCC	GGA	CGG	AGG	GAG	TAT	CAT	TTA	ACA	6048
	Ser	Ile	Ser	Ala	Thr	Ser	Ser	Ser	Gly	Arg	Arg	Glu	Tyr	His	Leu	Thr	
	2570						2575					2580					
5	AAT	ATA	TGC	ATG	TTC	GAA	GTA	AAT	CCC	CAC	GAA	TAA	GCA	TAT	AAG	ACG	6096
	Asn	Ile	Cys	Met	Phe	Glu	Val	Asn	Pro	His	Glu	*	Ala	Tyr	Lys	Thr	
	2585					2590					2595					2600	
10	ATA	TTG	CTT	TTT	GAC	TTG	CAA	CAC	CTA	AAC	CTC	ATT	GTT	TTC	TCC	TAG	6144
	Ile	Leu	Leu	Phe	Asp	Leu	Gln	His	Leu	Asn	Leu	Ile	Val	Phe	Ser	*	
					2605					2610					2615		
15	GAT	TTT	GGG	TGT	TCG	AAG	CAA	GCA	GCT	GGT	GAT	ATT	TAA	TTT	ACC	TTT	6192
	Asp	Phe	Gly	Cys	Ser	Lys	Gln	Ala	Ala	Gly	Asp	Ile	*	Phe	Thr	Phe	
				2620					2625					2630			
20	GCC	TTT	ATT	TGT	AGC	TTG	ATT	TGA	GGG	TGC	GGC	AAA	GGT	TTT	AGC	TTA	6240
	Ala	Phe	Ile	Cys	Ser	Leu	Ile	*	Gly	Cys	Gly	Lys	Gly	Phe	Ser	Leu	
			2635					2640						2645			
25	GTA	GTG	TTT	TGT	AAA	TTA	TTA	TAG	TTT	ATG	TAT	ATA	CTC	CTC	ATT	TGG	6288
	Val	Val	Phe	Cys	Lys	Leu	Leu	*	Phe	Met	Tyr	Ile	Leu	Leu	Ile	Trp	
			2650				2655					2660					
30	GCA	CTT	CCG	TAC	TGG	TCC	CAT	AGA	AGA	TAA	AAA	TGG	AAT	GAT	GTC	TGG	6336
	Ala	Leu	Pro	Tyr	Trp	Ser	His	Arg	Arg	*	Lys	Trp	Asn	Asp	Val	Trp	
	2665					2670					2675					2680	
35	CCA	ATA	ATT	GTT	GAC	AAC	ACT	GTT	GCG	CAT	TTG	ATT	TTT	ATC	AGG	GAA	6384
	Pro	Ile	Ile	Val	Asp	Asn	Thr	Val	Ala	His	Leu	Ile	Phe	Ile	Arg	Glu	
				2685						2690					2695		
40	TGG	AAA	ATT	GAA	ATC	GGT	AAG	AAA	CAT	TGC	GAT	ATT	AAG	CTT	GTA	TAT	6432
	Trp	Lys	Ile	Glu	Ile	Gly	Lys	Lys	His	Cys	Asp	Ile	Lys	Leu	Val	Tyr	
			2700					2705						2710			
45	GCT	AAT	GCT	GGT	GGA	TCT	TTA	AGA	GGG	AAC	ATA	TGA	TCT	CGT	GTG	CAT	6480
	Ala	Asn	Ala	Gly	Gly	Ser	Leu	Arg	Gly	Asn	Ile	*	Ser	Arg	Val	His	
			2715					2720					2725				
50	CCA	TCT	TCA	ACT	AAA	AAA	ATA	TGT	TGC	ACA	TCT	CCC	ACG	TCA	CTT	ACT	6528
	Pro	Ser	Ser	Thr	Lys	Lys	Ile	Cys	Cys	Thr	Ser	Pro	Thr	Ser	Leu	Thr	
			2730				2735					2740					
55	AGC	TAT	TTC	ATC	CAA	GTA	CTA	ACT	TGT	GTG	GTT	GTC	TCC	TCA	GTA	CCG	6576
	Ser	Tyr	Phe	Ile	Gln	Val	Leu	Thr	Cys	Val	Val	Val	Ser	Ser	Val	Pro	
	2745					2750					2755					2760	
60	GGA	CAT	TGT	GCG	CCA	ATT	CAT	TAA	AGG	CAC	TGA	TGG	ATT	TGC	TGG	TGG	6624
	Gly	His	Cys	Ala	Pro	Ile	His	*	Arg	His	*	Trp	Ile	Cys	Trp	Trp	
				2765					2770						2775		
65	TTT	TGC	CGA	ATG	TCT	TTG	TGG	AAG	TCC	ACA	CCT	ATA	CCA	GGT	AAG	TTG	6672
	Phe	Cys	Arg	Met	Ser	Leu	Trp	Lys	Ser	Thr	Pro	Ile	Pro	Gly	Lys	Leu	
				2780					2785					2790			
70	TGG	CAA	TAC	TTG	GAA	ATG	GGT	TGA	GTG	AAT	GTC	ACA	TGG	ATT	TTT	TAT	6720
	Trp	Gln	Tyr	Leu	Glu	Met	Gly	*	Val	Asn	Val	Thr	Trp	Ile	Phe	Tyr	
			2795					2800					2805				
75	ATA	TAC	CAC	ATG	ATG	ATA	CAC	ATG	TAA	ATA	TAT	AAC	GAT	TAT	AGT	GTA	6768
	Ile	Tyr	His	Met	Met	Ile	His	Met	*	Ile	Tyr	Asn	Asp	Tyr	Ser	Val	
		2810					2815					2820					

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	TGC ATA TGC ATT TGG CTA AGA AGT ACT CCC TCC CTT AGT AAA AGT TAG	6816
	Cys Ile Cys Ile Trp Leu Arg Ser Thr Pro Ser Leu Ser Lys Ser *	
	2825 2830 2835 2840	
5	TAC AAA GTT GAG TCA TCT ATT TTG GAA CGG AGG GAG TAT AAG TGT ATA	6864
	Tyr Lys Val Glu Ser Ile Leu Glu Arg Arg Glu Tyr Lys Cys Ile	
	2845 2850 2855	
10	CAC TAG TGC AAT ATA TAG GTT TTA ACA CCC AAC TTG CCA ATG AAG GAA	6912
	His * Cys Asn Ile * Val Leu Thr Pro Asn Leu Pro Met Lys Glu	
	2860 2865 2870	
15	CAT AGG GCT TTC TAG TTA TCT TAT TTA TTT GTC TGG TGA ATA ATC CAC	6960
	His Arg Ala Phe * Leu Ser Tyr Leu Phe Val Trp * Ile Ile His	
	2875 2880 2885	
20	TGA AAA ATT CCA GCC ATG TCA TTT TTT AGG GGG GGA GAA GAA ACT ACA	7008
	* Lys Ile Pro Ala Met Ser Phe Phe Arg Gly Gly Glu Glu Thr Thr	
	2890 2895 2900	
25	TTG ATT TTT CCC CCT AAA AAA AGC CAT CTC AGA TTT CAT AGG TAA CTT	7056
	Leu Ile Phe Pro Pro Lys Lys Ser His Leu Arg Phe His Arg * Leu	
	2905 2910 2915 2920	
30	GCT TTT CTG TAA AGA AAT GAA AAC GAC TTC ATA CTT TCT GTC GAT TAT	7104
	Ala Phe Leu * Arg Asn Glu Asn Asp Phe Ile Leu Ser Val Asp Tyr	
	2925 2930 2935	
35	AAG TGT ATA CAC TAG TGC AAT ATA TAG GTT TTA ACA CCC AAC TTG CCA	7152
	Lys Cys Ile His * Cys Asn Ile * Val Leu Thr Pro Asn Leu Pro	
	2940 2945 2950	
40	ATG AAG GAA CAT AGG GCT TTC TAG TTA TCT TAT TTA TTT GCT GGT GAA	7200
	Met Lys Glu His Arg Ala Phe * Leu Ser Tyr Leu Phe Ala Gly Glu	
	2955 2960 2965	
45	TAA TCC ACT GAA AAA TTC CAG CCA TGT CAT TTT TTA GGG GGG AGA AGA	7248
	* Ser Thr Glu Lys Phe Gln Pro Cys His Phe Leu Gly Gly Arg Arg	
	2970 2975 2980	
50	AAC TAT ATT GAT TTT TCC CCC TAA AAA AAG CCA TCT CAG ATT CAT AGG	7296
	Asn Tyr Ile Asp Phe Ser Pro * Lys Lys Pro Ser Gln Ile His Arg	
	2985 2990 2995 3000	
55	AAC TTG CTT TTC TGT AAA GAA ATG AAA ACG ACT TCA TAC TTT CTG CGG	7344
	Asn Leu Leu Phe Cys Lys Glu Met Lys Thr Thr Ser Tyr Phe Leu Arg	
	3005 3010 3015	
60	CGC TTA CTT AGC TCG ATG GAT ATT TGT AAG ATG AAT GCC AAA TTA TTT	7392
	Arg Leu Leu Ser Met Asp Ile Cys Lys Met Asn Ala Lys Leu Phe	
	3020 3025 3030	
65	GGC GGG ATT TGA TCG TTA TTC CAA ATT TCA TTT GGT TTC TCT AGC AAT	7440
	Gly Gly Ile * Ser Leu Phe Gln Ile Ser Phe Gly Phe Ser Ser Asn	
	3035 3040 3045	
70	CAA CCC AGT ACC TTG TTA TTG GCA CTG CAA TTT CTT ATT GAT TAA TCA	7488
	Gln Pro Ser Thr Leu Leu Leu Ala Leu Gln Phe Leu Ile Asp * Ser	
	3050 3055 3060	
75	GGC AGG AGG AAG GAA ACC TTG GCA CAG TAT CAA CTT GGT ATG TGC ACA	7536
	Gly Arg Arg Lys Glu Thr Leu Ala Gln Tyr Gln Leu Gly Met Cys Thr	
	3065 3070 3075 3080	

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	TGA TGG ATT TAC ACT GGG TGA TTT GGT ACA TAT AAT ACC AAG TCA ATT	7584
	* Trp Ile Tyr Thr Gly * Phe Gly Thr Tyr Asn Thr Lys Ser Ile	
	3085 3090 3095	
5	TAC CAA ATG GGG AGA CCA ATA GAG ATG GAG AAA ATC ACA ATC TTA GCT	7632
	Tyr Gln Met Gly Arg Pro Ile Glu Met Glu Lys Ile Thr Ile Leu Ala	
	3100 3105 3110	
10	GGA ATT GTG GGG AGG TAA TTC TGA ACT CTC CTT TTT TTT TGA AAT TTT	7680
	Gly Ile Val Gly Arg * Phe * Thr Leu Leu Phe Phe * Asn Phe	
	3115 3120 3125	
15	CAT GCT TTA CAT AAT AGT CAA ATG GCT GAC AAA TGT CGT TGT ATG GTT	7728
	His Ala Leu His Asn Ser Gln Met Ala Asp Lys Cys Arg Cys Met Val	
	3130 3135 3140	
20	CTC TCT ACC TAA ACC GTT AAG GCA GTA AGA GTT TCC CTA CAA GAT CTC	7776
	Leu Ser Thr * Thr Val Lys Ala Val Arg Val Ser Leu Gln Asp Leu	
	3145 3150 3155 3160	
	TTT GTT CGT ATA ATT GTA TTT TCT AGA GAA AAG TTG CCT TCA ATT TTG	7824
	Phe Val Arg Ile Ile Val Phe Ser Arg Glu Lys Leu Pro Ser Ile Leu	
	3165 3170 3175	
25	TGC ACG CGG CAG TAC AGG AAT TGT GGT TAT AAA TAT TGA TAC AGG CTG	7872
	Cys Thr Arg Gln Tyr Arg Asn Cys Gly Tyr Lys Tyr * Tyr Arg Leu	
	3180 3185 3190	
30	ACC ATC GTT ACT AAT AGG GGG AAC AAT AAG CAC ATT TTT TTA ATA GCA	7920
	Thr Ile Val Thr Asn Arg Gly Asn Asn Lys His Ile Phe Leu Ile Ala	
	3195 3200 3205	
35	AAG GCA TCA CCC TTG TTC CGT TTC CAA TGA AAT CAC AGT ATC CGA ACC	7968
	Lys Ala Ser Pro Leu Phe Arg Phe Gln * Asn His Ser Ile Arg Thr	
	3210 3215 3220	
40	ATA AGT TTT ACA AGT ATG CGT AGA GAG AAA TAA AGT ATC AAC CCG GCA	8016
	Ile Ser Phe Thr Ser Met Arg Arg Glu Lys * Ser Ile Asn Pro Ala	
	3225 3230 3235 3240	
	GAA ACA GTT GTT TCA GGC GCA AAG AGA AAA GGA AAC GAT ATG CTC TAT	8064
	Glu Thr Val Val Ser Gly Ala Lys Arg Lys Gly Asn Asp Met Leu Tyr	
	3245 3250 3255	
45	TAC ATC AAC CTT TTA GCA TTT AGG GAC GAC CAG CAT CAT CCC ATC TTC	8112
	Tyr Ile Asn Leu Leu Ala Phe Arg Asp Asp Gln His His Pro Ile Phe	
	3260 3265 3270	
50	AAT CAA CTG GAG CGA GGT CAC CTC CAA TCT TCT CAG CAG CCT CAG AGT	8160
	Asn Gln Leu Glu Arg Gly His Leu Gln Ser Ser Gln Gln Pro Gln Ser	
	3275 3280 3285	
55	GGT GAC CTC CCA AGC AAG TGC ATC AGC ATC CAT CAT CTG GGG GTT GGG	8208
	Gly Asp Leu Pro Ser Lys Cys Ile Ser Ile His His Leu Gly Val Gly	
	3290 3295 3300	
60	CAC ATA CCA TGA GCA CAA TCA CCT GAA TTT GAT GAA TTT TCC TCT GTT	8256
	His Ile Pro * Ala Gln Ser Pro Glu Phe Asp Glu Phe Ser Ser Val	
	3305 3310 3315 3320	
	TAC CTT GCA GCA GAC CCC TGC CGT ATA AAT GGT TTT AAA TGA CAG CAT	8304
	Tyr Leu Ala Ala Asp Pro Cys Arg Ile Asn Gly Phe Lys * Gln His	
	3325 3330 3335	

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	GTT	CTT	TCA	GTT	TGA	GCA	AAA	TTT	GTG	CAA	TTG	CAA	AGA	AGC	TTT	AGA	8352
	Val	Leu	Ser	Val	*	Ala	Lys	Phe	Val	Gln	Leu	Gln	Arg	Ser	Phe	Arg	
				3340					3345					3350			
5	ATC	ATG	TGG	AAC	ATG	CAC	TTA	CAT	TTC	ATC	TGA	CAA	TAT	AGG	AAG	GAG	8400
	Ile	Met	Trp	Asn	Met	His	Leu	His	Phe	Ile	*	Gln	Tyr	Arg	Lys	Glu	
			3355				3360						3365				
10	AGC	CCG	ACG	TCG	CAT	GCT	CCT	CTA	GAC	TCG	AGG	AAT	TCG	CAA	GAT	TGT	8448
	Ser	Pro	Thr	Ser	His	Ala	Pro	Leu	Asp	Ser	Arg	Asn	Ser	Gln	Asp	Cys	
		3370					3375					3380					
15	CTG	TCA	AAA	GAT	TGA	GGA	AGA	GGC	AGA	TGC	GCA	ATT	TCT	TTG	TTT	GTC	8496
	Leu	Ser	Lys	Asp	*	Gly	Arg	Gly	Arg	Cys	Ala	Ile	Ser	Leu	Phe	Val	
	3385					3390				3395						3400	
20	TCA	TGG	TTT	CTC	AAG	TAA	GAC	TTA	TAT	CTG	ATC	TCT	TCA	ATT	TTT	GAG	8544
	Ser	Trp	Phe	Leu	Lys	*	Asp	Leu	Tyr	Leu	Ile	Ser	Ser	Ile	Phe	Glu	
				3405						3410					3415		
25	ATT	GCC	TGT	TTT	TCA	CAA	TGG	CAT	ATG	TTG	TCA	GGT	GAA	ACA	TCC	AAT	8592
	Ile	Ala	Cys	Phe	Ser	Gln	Trp	His	Met	Leu	Ser	Gly	Glu	Thr	Ser	Asn	
				3420					3425					3430			
30	CCC	AGT	ATT	AAT	AGA	GCC	AAC	ATG	AAG	GGA	TTG	CTT	ATC	TGA	GAT	ATC	8640
	Pro	Ser	Ile	Asn	Arg	Ala	Asn	Met	Lys	Gly	Leu	Leu	Ile	*	Asp	Ile	
			3435					3440					3445				
35	TGC	CAA	AGT	TGA	ATT	CTT	AGA	TTC	ACC	TTC	TTC	AGT	ATT	TCA	GAC	CTT	8688
	Cys	Gln	Ser	*	Ile	Leu	Arg	Phe	Thr	Phe	Phe	Ser	Ile	Ser	Asp	Leu	
		3450				3455						3460					
40	CTA	AGC	ATT	TTC	ATT	TTT	TTT	TTC	AAT	TGT	TAG	GGA	GTT	CCA	ATG	TTT	8736
	Leu	Ser	Ile	Phe	Ile	Phe	Phe	Phe	Asn	Cys	*	Gly	Val	Pro	Met	Phe	
	3465					3470				3475						3480	
45	TAC	ATG	GGC	GAT	GAA	TAT	GGC	CAC	ACA	AAA	GGG	GGC	AAC	AAC	AAT	ACA	8784
	Tyr	Met	Gly	Asp	Glu	Tyr	Gly	His	Thr	Lys	Gly	Gly	Asn	Asn	Asn	Thr	
				3485						3490					3495		
50	TAC	TGC	CAT	GAT	TCT	TAT	GTC	AGT	ACA	ATT	TGG	TCA	CAT	ATT	GTT	GTT	8832
	Tyr	Cys	His	Asp	Ser	Tyr	Val	Ser	Thr	Ile	Trp	Ser	His	Ile	Val	Val	
				3500				3505						3510			
55	CTA	AGT	AAC	TAT	CTT	CAA	ATC	TTT	GCA	TTC	ATC	CGT	CAT	GGC	TCT	TCT	8880
	Leu	Ser	Asn	Tyr	Leu	Gln	Ile	Phe	Ala	Phe	Ile	Arg	His	Gly	Ser	Ser	
			3515				3520					3525					
60	GTA	GGT	CAA	TTA	TTT	TCG	CTG	GGA	TAA	AAA	AGA	ACA	ATA	CTC	TGA	CTT	8928
	Val	Gly	Gln	Leu	Phe	Ser	Leu	Gly	*	Lys	Arg	Thr	Ile	Leu	*	Leu	
		3530					3535				3540						
65	GCA	AAG	ATT	CTG	CTG	CCT	CAT	GAC	CAA	ATT	CCG	CAA	GTA	AGT	ATT	CCG	8976
	Ala	Lys	Ile	Leu	Leu	Pro	His	Asp	Gln	Ile	Pro	Gln	Val	Ser	Ile	Pro	
	3545					3550					3555					3560	
70	TTG	AAT	AAT	TTC	TGT	GTA	GAA	CCA	CTG	AAG	GTG	CCT	CCA	AAC	GCT	AAG	9024
	Leu	Asn	Asn	Phe	Cys	Val	Glu	Pro	Leu	Lys	Val	Pro	Pro	Asn	Ala	Lys	
				3565					3570					3575			
75	CGA	GCA	AGG	TCA	ATT	TCA	CAC	CCT	AAT	CAA	GTT	GGT	GTT	GTC	TAT	TTG	9072
	Arg	Ala	Arg	Ser	Ile	Ser	His	Pro	Asn	Gln	Val	Gly	Val	Val	Tyr	Leu	
			3580					3585						3590			

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	TGT ATT TGA TCT GCT GCA CTG TAG GGA GTG CGA GGG TCT TGG CCT TGA	9120
	Cys Ile * Ser Ala Ala Leu * Gly Val Arg Gly Ser Trp Pro *	
	3595 3600 3605	
5	GGA CTT TCC AAC GGC CGA ACG GCT GCA GTG GCA TGG TCA TCA GCC TGG	9168
	Gly Leu Ser Asn Gly Arg Thr Ala Ala Val Ala Trp Ser Ser Ala Trp	
	3610 3615 3620	
10	GAA GCC TGA TTG GTC TGA GAA TAG CCG ATT CGT TGC CTT TTC CAT GGT	9216
	Glu Ala * Leu Val * Glu * Pro Ile Arg Cys Leu Phe His Gly	
	3625 3630 3635 3640	
15	ACA CAT ATA GTT CTG ACA CTT CAC TAT AGT TGT TTT AAA AAA GAA AAT	9264
	Thr His Ile Val Leu Thr Leu His Tyr Ser Cys Phe Lys Lys Glu Asn	
	3645 3650 3655	
	TTA ACT CAA AAG TAA ATT ATG GAG A	9289
	Leu Thr Gln Lys * Ile Met Glu	
	3660	

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